

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2004, 23:42:47 ; Search time 2250 Seconds
(without alignments)
10267.483 Million cell updates/sec

Title: US-10-623-891-2
Perfect score: 533
Sequence: 1 tctggaggaggagctccg999.....cgtgagtttcggtacacaa 533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapest 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl : *

1: gb_ba:*

2: gb_hlg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_ov:*

21: em_or:*

22: em_ov:*

23: em_pac:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hlg_hum:*

31: em_hlg_inv:*

32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_rtd:*

36: em_hlg_mam:*

37: em_hlg_vrt:*

38: em_hlg_hum:*

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40: em_hlg_hum:*

41: em_hlg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	100.0	585	14	S82226
2	507.8	95.3	1005	14	ACRLTR1
3	506	94.9	4232	14	AF006065
4	506	94.9	8221	14	AF246698
5	503	94.4	887	14	ACRLTR2
6	490.8	92.1	745	14	AY255632
7	439.4	82.4	940	6	BD006232
8	438.4	82.3	545	14	S70398
9	429	80.5	583	14	S79845
10	313.8	58.9	859	14	REXX2
11	313.8	58.9	891	14	REXX1
12	206.4	38.7	1032	14	AF006066
13	193	36.2	465	14	AY255633
14	193	36.2	2640	14	AF006064
15	193	36.2	288539	14	AF198100
16	155	29.1	578	6	A83549
17	155	29.1	578	6	BD006233
18	130.4	24.5	1530	14	RESNVX
19	119.6	22.4	160	5	CHKSNTV12
20	119.6	22.4	160	5	CHKSNTV12
21	119.6	22.4	160	5	CHKSNTV12
22	119.6	22.4	160	5	CHKSNTV12
23	119.6	22.4	160	5	CHKSNTV12
24	119.6	22.4	160	5	CHKSNTV12
25	119.6	22.4	160	5	CHKSNTV12
26	106.2	19.9	180	14	SNVTR
27	80.8	15.2	163	14	SNVTRTMB
28	64.8	12.2	100	14	SNVTR12
29	58.4	11.0	209	14	SNVTRTMA
30	44.8	8.4	69	5	CHKSNTV1
31	42.6	8.0	63	5	CHKSNTV1
32	42.6	8.0	69	5	CHKSNTV1
33	42.6	8.0	69	5	CHKSNTV1
34	42.2	7.9	69	5	CHKSNTV1
35	42.2	7.9	69	5	CHKSNTV1
36	40.4	7.6	100	14	SNVTR11
37	39.6	7.4	155853	5	AL935041
38	39.6	7.4	167563	5	AL928838
39	39.6	7.4	182325	5	BX004869
40	39.6	7.4	189694	2	BX005365
41	39.6	7.4	207161	2	BX530067
42	39.6	7.4	211383	2	BX119319
43	39.6	7.4	219981	2	BX544872
44	39.6	7.4	224806	2	BX004858
45	39.2	7.4	237323	10	AL772376

ALIGNMENTS

RESULT 1

LOCUS S82226 585 bp DNA linear VRL 12-FEB-1997

DEFINITION (RS region, intervening sequence) [Marek's disease virus MDV, RML, Genomic DNA, 585 nt].

ACCESSION S82226

VERSION S82226.1 GI:1639499

KEYWORDS

SOURCE Gallid herpesvirus 2

ORGANISM Gallid herpesvirus 2

REFERENCE 1 (bases 1 to 585)

AUTHORS Alphanherpesvirinae; Marek's disease-like viruses.

TITLE 'Retroviral'-inertional-activation-in-a-herpesvirus-transcriptional

Pred. No. is the number of results predicted by chance to have a

activation of US genes by an integrated long terminal repeat in a Marek's disease virus clone
J. Virol. 70 (4), 2460-2467 (1996)

JOURNAL
MEDLINE
PUBMED
REMARK

GenBank staff at the National Library of Medicine created this entry [NCBI gi18131] from the original journal article.

COMMENT

Authors indicate intervening sequence from nt 23 to nt 555 inclusive derived from co-infecting reticuloendotheliosis virus strain CSV.

FEATURES

source location/Qualifiers

1..585
/organism="Gallid herpesvirus 2"
/mol_type="genomic DNA"
/db_xref="taxon:10390"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 533; DB 14; Length 585;

Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGTGGAGGAGAGCTCGGGGAGATGAGGAGAGAGCTCGGGGAGATAGCGCTGCTCG 60

23 TGTGGAGGAGAGCTCGGGGAGATGAGGAGAGAGCTCGGGGAGATAGCGCTGCTCG 82

61 CTACTGCGCATTTAGCTTCTGTAATCATGCTTCTGCTTACCGGCTTGTACTTGA 120

83 CTACTGCGCATTTAGCTTCTGTAATCATGCTTCTGCTTACCGGCTTGTACTTGA 142

121 TATATTTGCTGATTCATTTCTCGGATTCGAGATCAGACAGGCTCATTAACCATAA 180

143 TATATTTGCTGATTCATTTCTCGGATTCGAGATCAGACAGGCTCATTAACCATAA 202

181 AGGAATGTTGTTGAGGAGAGATCAGACAGGCTCATTAACCATTAACAACA 240

203 AGGAATGTTGTTGAGGAGAGATCAGACAGGCTCATTAACCATTAACAACA 262

241 CGAGATCGACATTCATTCAGGAGATGTTGTTGAGGAGATGTTGTTGTTGTTGTTG 300

263 CGAGATCGACATTCATTCAGGAGATGTTGTTGAGGAGATGTTGTTGTTGTTGTTG 322

301 GGGAAATGTCATCAATCTGTAAAGCGGCTTATTAAGCGAGTCTCTTGTCTG 360

323 GGGAAATGTCATCAATCTGTAAAGCGGCTTATTAAGCGAGTCTCTTGTCTG 382

361 GGGGCGGCGCTCAATCTGTAAAGCGGCTTATTAAGCGAGTCTCTTGTCTG 420

383 GGGGCGGCGCTCAATCTGTAAAGCGGCTTATTAAGCGAGTCTCTTGTCTG 442

421 TTTTCTTCTATATCTCAATCTGTAAAGCGGCTTATTAAGCGAGTCTCTTGTCTG 480

443 TTTTCTTCTATATCTCAATCTGTAAAGCGGCTTATTAAGCGAGTCTCTTGTCTG 502

481 CTTACTGCGGAGGAGATCCGAGCTGAATCCGTAATTTTGGTACACA 533

503 CTTACTGCGGAGGAGATCCGAGCTGAATCCGTAATTTTGGTACACA 555

RESULT 2

ACRLTRI 1005 bp ss-RNA linear VRL 27-APR-1993

LOCUS Reticuloendotheliosis virus 713 proviral clone RNA.

DEFINITION M22223 M10659 M16722

VERSION M22223.1 GI:209708

KEYWORDS long terminal repeat (LTR).

SOURCE Reticuloendotheliosis virus

ORGANISM Reticuloendotheliosis virus

REFERENCE 1 (bases 99 to 195)

Authors Ridgway,A., Swift,R.A., Kung,H.J., and Fujita,D.J.

In vitro transcription analysis of the viral promoter involved in

c-myc activation in chicken B lymphomas: detection and mapping of

two RNA initiation sites within the reticuloendotheliosis virus

long terminal repeat

J. Virol. 54 (1), 161-170 (1985)

JOURNAL MEDLINE PUBMED

REFERENCE 2 (bases 1 to 1005)

Authors Swift,R.A., Boerkoel,C., Ridgway,A., Fujita,D.J., Dodgson,J.B. and

Kung,H.J.

B-lymphoma induction by reticuloendotheliosis virus:

characterization of a mutated chicken syncytial virus provirus

involved in c-myc activation

J. Virol. 61 (7), 2084-2090 (1987)

JOURNAL MEDLINE PUBMED

COMMENT Original source text: Reticuloendotheliosis virus (from chicken

ORIGIN

19 bp upstream of SacI site.

LTR

Query Match 95.3%; Score 507.8; DB 14; Length 1005;

Best Local Similarity 99.6%; Pred. No. 2,9e-145;

Matches 509; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

23 ATGTGGAGGAGAGCTCGGGGAGATGAGGAGAGAGCTCGGGGAGATAGCGCTTCTG 82

5 ATGTGGAGGAGAGCTCGGGGAGATGAGGAGAGAGCTCGGGGAGATAGCGCTTCTG 64

83 TATATGCTTCTGCTTCTGCTTACCGGCTTGTACTTGTATATTTCCGTATATCTTC 142

65 TATATGCTTCTGCTTCTGCTTACCGGCTTGTACTTGTATATTTCCGTATATCTTC 124

143 TCGGAATCGGAGATCAAGAGAGGCTCATTAACCATTAAGGAATGTTGTTGAGGCAA 202

125 TCGGAATCGGAGATCAAGAGAGGCTCATTAACCATTAAGGAATGTTGTTGAGGCAA 184

203 GCATCAAGCACTTGACATTCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 262

185 GCATCAAGCACTTGACATTCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 244

263 GCGAATGTTGTTGAGGAGATGCTATCTTCCATGAGGAGGAATGCTATGCAATCC 322

245 GCGAATGTTGTTGAGGAGATGCTATCTTCCATGAGGAGGAATGCTATGCAATCC 304

323 TGTAAAGCGGCTATTAAGCAAGAGTGCATCTTGTCTCGGGGTGCGGCTCTACATTTG 382

305 TGTAAAGCGGCTATTAAGCAAGAGTGCATCTTGTCTCGGGGTGCGGCTCTACATTTG 364

383 TGTAAAGCGGCTATTAAGCAAGAGTGCATCTTGTCTCGGGGTGCGGCTCTACATTTG 442

365 TGTAAAGCGGCTATTAAGCAAGAGTGCATCTTGTCTCGGGGTGCGGCTCTACATTTG 424

443 TGTAAAGCGGCTATTAAGCAAGAGTGCATCTTGTCTCGGGGTGCGGCTCTACATTTG 502

425 TGTAAAGCGGCTATTAAGCAAGAGTGCATCTTGTCTCGGGGTGCGGCTCTACATTTG 484

503 CGGACTGAATCCGTAGTATTTGGTACACA 533

485 CGGACTGAATCCGTAGTATTTGGTACACA 515

RESULT 3

AF006065 4292 bp DNA linear VRL 16-SEP-1997

LOCUS Fowlpox virus 8 gag gene, complete cds, and protease/polymerase

DEFINITION (pro/pol) gene, partial cds.

VERSION AF006065

ACCESSION AF006065

REFERENCE 1 GI:2393892

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Fowlpox virus
Fowlpox virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Avipoxvirus.
1 (bases 1 to 4292)
Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated
sequences from the avian retrovirus, reticuloendotheliosis virus
Virology 235 (2), 367-376 (1997)
97428585
9281517
2 (bases 1 to 4292)
Hertig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.B.
Direct Submission
Submitted (30-MAY-1997) Division of Animal Health, CSIRO, 5
Portarlington Road, Geelong, Victoria 3213, Australia
Location/Qualifiers
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/mol_type="genomic DNA"
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Ltd, Castle Hill, New South Wales, Australia.
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Integrated reticuloendotheliosis virus"
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Query Match	Similarity	94.9%; Score 506; DB 14; Length 4297;
Best Local	Similarity	100.0%; Prod. No. 1,je-144;
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OY	28	GAGGAGAGCTCCGGGGGAATAGCGCTGCCTCCTAACCTGCCATATTAGCTTCTGTATTC 87
DB	908	CGAGGAGACTCCGGGGGAATAGCGCTGCCTCCTAACCTGCCATATTAGCTTCTGTATTC 967
OY	88	ATGCTTGTTGCCCTTAGACCCCATTTGTAATCTGATAATATTTCGGTGATATATCAATTTCTCGGA 147
DB	968	ATGCTTGTTGCCCTTAGACCCCATTTGTAATCTGATAATATTTCGGTGATATATCAATTTCTCGGA 1027
OY	148	ATCGGCATCAAGAGAGAGCTCATTAACCAATPAAGAATGTTGTTGAAGGCAAGCATC 207
DB	1028	ATCGGCATCAAGAGAGAGCTCATTAACCAATPAAGAATGTTGTTGAAGGCAAGCATC 1087
OY	208	AGACCACCTTGACCACTCAATCAATCAAGAAACAACAAGATCGAATCATATCACTAGSCAA 267
DB	1088	AGACCACCTTGACCACTCAATCAATCAAGAAACAACAAGATCGAATCATATCACTAGSCAA 1147
OY	268	TGTTGTTAAAGGAGAGATGCTATTCCTCCATAGAGGAAAATGTATGACACATCTCTGTA 327
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DB	1208	GCGGCTAATPAPAGCAGGTGCATCTTGTCTCGGGGGTCGCGGCTCACATGTTGTNGA 1267
OY	388	CGTCGCGGCCAGATTCGATCTGTATATAAAGCTTTTCTCTATATCTTCAGATTGGCA 447
DB	1268	CGTCGCGGCCAGATTCGATCTGTATATAAAGCTTTTCTCTATATCTTCAGATTGGCA 1327
OY	448	GTAAGAGAGATTTTTGTTCTGTGTGTTGGCTGCGCTTACTGGTGGGGTAGGAGATCCGGAC 507
DB	1328	GTAAGAGAGATTTTTGTTCTGTGTGTTGGCTGCGCTTACTGGTGGGGTAGGAGATCCGGAC 1387
OY	508	TGAATCCGTACTATTTCGGTACACA 533
DB	1388	TGAATCCGTACTATTTCGGTACACA 1413
RESULT 4		
AF246698		
LOCUS	AF246698	8221 bp DNA linear VRL 12-MAR-2003
DEFINITION	Fowlpox virus hypothetical protein gene, partial cds; integrated reiculoendocheliosis provirus, complete sequence; and protein kinase-like protein gene, partial cds.	
VERSION	AF246698	
KEYWORDS	AF246698.2 GI:28927668	
SOURCE ORGANISM	Fowlpox virus Fowlpox virus Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.	
REFERENCE AUTHORS	1 (bases 1 to 8221) Singh, P., Kim, T.-J. and Tripathy, D.N. Re-emerging fowlpox: evaluation of isolates from vaccinated flocks Avian Pathol. 29, 449-455 (2000)	
JOURNAL TITLE	2 (bases 1 to 8221) Singh, P., Schitzlein, W.M. and Tripathy, D.N. Reiculoendocheliosis Virus Sequences Within the Genomes of Field Strains of Fowlpox Virus Display Variability J. Virol. (2003) In press	
REFERENCE AUTHORS	3 (bases 1 to 8221) Schitzlein, W.M., Srinivasan, V. and Tripathy, D.N. Direct Submission Submitted (16-MAR-2000) Veterinary Pathobiology, University of Illinois, Illinois, 2001 South Lincoln Avenue, Urbana, IL 61802, USA	
JOURNAL TITLE	4 (bases 1 to 8221) Schitzlein, W.M., Singh, P., Srinivasan, V. and Tripathy, D.N. Direct Submission Submitted (12-MAR-2003) University of Illinois at Urbana-Champaign, Urbana, IL 61802, USA	
REFERENCE AUTHORS	2001 South Lincoln Avenue, Urbana, IL 61802, USA	
JOURNAL TITLE		

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REMARK      Sequence update by submltiter
COMMENT      On Mar 12, 2003 this sequence version replaced gi:8926141.
FEATURES
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ORIGIN
Query Match      94.9%; Score 506; DB 14; Length 8221;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/translation="MDCLTNLSABGKVDQAQKTLILVVMNGFTAGVPLQOLMG
LPDCSGGYVFSIPITYNSLDGSSSTALVTGSGSGMGMGSGRQOEVCYFKKI
PSVOQGPCEPSECLITATOMSTCEKROECTLKYFTAILOKTLGSLIEDPNK
LLOASCTGKNGKVCMDPVAIPVYVSGGPTMIBESVREBLEETIRHSYPSVYHP
LALPRGVLDLPQSDIIEATHQVLANATNPOLAEKWCMLTGTPPIPAALPANVNT
LNBKCSLSLPRFVQPTGSIDVNCYAGEANRNGIPLGVHFPNCTSLIEVNSHIR
NLTPLCPFGVHVCNNNAVYALPKNMTGLCISLIVDMSIISGEEPIPLPSLEYT
AGNRKRAVOFIPLVGLGTTGATLAGTGLGVSVHTYHKLSQLIEDVOALSGTNDL
ODQIDSLAVVLQNRBGDILLTAEOGICLALQECFPYANSGLIVRKIRLQEDLI
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/codon_start=1
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/protein_id="AA062319.1"
/db_xref="GI:28927673"
/translation="MDITNTMPDIQNDIPNIPYDIERPLVYS"

LTR
CDS
/translation="MDCLTNLSABGKVDQAQKTLILVVMNGFTAGVPLQOLMG
LPDCSGGYVFSIPITYNSLDGSSSTALVTGSGSGMGMGSGRQOEVCYFKKI
PSVOQGPCEPSECLITATOMSTCEKROECTLKYFTAILOKTLGSLIEDPNK
LLOASCTGKNGKVCMDPVAIPVYVSGGPTMIBESVREBLEETIRHSYPSVYHP
LALPRGVLDLPQSDIIEATHQVLANATNPOLAEKWCMLTGTPPIPAALPANVNT
LNBKCSLSLPRFVQPTGSIDVNCYAGEANRNGIPLGVHFPNCTSLIEVNSHIR
NLTPLCPFGVHVCNNNAVYALPKNMTGLCISLIVDMSIISGEEPIPLPSLEYT
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ODQIDSLAVVLQNRBGDILLTAEOGICLALQECFPYANSGLIVRKIRLQEDLI
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7804. .8053
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/notes="ORF 203"
/codon_start=1
/product="protein kinase-like protein"
/protein_id="AA062319.1"
/db_xref="GI:28927673"
/translation="MDITNTMPDIQNDIPNIPYDIERPLVYS"

RESULT 5
ACRLTR2      887 bp ss-RNA      linear      VRL 27-APR-1993
LOCUS        Reticuloendotheliosis virus 713 proviral clone RNA.
DEFINITION   M22224 M10660 M16722
ACCESSION    M22224.1 GI:209709
VERSION      M22224.1 GI:209709
KEYWORDS     long terminal repeat (LTR).
SOURCE       Reticuloendotheliosis virus
ORGANISM     Reticuloendotheliosis virus
REFERENCE    1 (bases 510 to 602)
Viruses; Retroviridae; Gammaretrovirus.
```

AUTHORS Ridgway,A.A., Swift,R.A., Kung,H.J. and Fujita,D.J.
TITLE In vitro transcription analysis of the viral promoter involved in c-myc activation in chicken B lymphomas: detection and mapping of two RNA initiation sites within the reticuloendotheliosis virus long terminal repeat
JOURNAL J. Virol. 54 (1), 161-170 (1985)
MEDLINE 85135063
PUBMED 2983111
REFERENCE 2 (bases 1 to 887)
AUTHORS Swift,R.A., Boerkoel,C., Ridgway,A., Fujita,D.J., Dodgson,J.B. and Kung,H.J.
TITLE B-lymphoma induction by reticuloendotheliosis virus: characterization of a mutated chicken syncytial virus provirus involved in c-myc activation
JOURNAL J. Virol. 61 (7), 2084-2090 (1987)
MEDLINE 8726389
PUBMED 3035210
COMMENT Original source text: Reticuloendotheliosis virus (from chicken line 151-5 B lymphomas), cDNA to mRNA, clone 713.
FEATURES
 source
 1..887
 /organism="Reticuloendotheliosis virus"
 /mol_type="Genomic RNA"
 /db_xref="taxon:11636"
 246..750
 LTR
 /note="3' LTR"
 misc_feature
 805..806
 /note="cryptic intron splice donor site"
 ORIGIN About 700 bp after segment 1.
 Query Match 94.4%; Score 503; DB 14; Length 887;
 Best Local Similarity 99.0%; Pred. No. 8.8e-14; Mismatches 5; Indels 0; Gaps 0;
 Matches 506; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 23 ATGTGGAGGAGAGCTCCGGGGGAGATAGCGCTGCTGCTACTGACATATTAGCTTCTG 82
 DB 245 ATGTGGAGGAGAGCTCCGGGGGAGATAGCGCTGCTGCTACTGACATATTAGCTTCTG 304
 QY 83 TAATCATGCTTGTGCTTACCGCCGATTTGATTAATTTTGGCTGATATCTTC 142
 DB 305 TAATCATGCTTGTGCTTACCGCCGATTTGATTAATTTTGGCTGATATCTTC 364
 QY 143 TCGGAATCGGCATCAAGAGAGGCTCATTAACCAATAAGGAATGTTGTGAAGCAA 202
 DB 365 TCGGAATCGGCATCAAGAGAGGCTCATTAACCAATAAGGAATGTTGTGAAGCAA 424
 QY 203 GCATCAGACCACTTGCATCCATCAATCAAGAAACAGAGATGAACTATCACTGA 262
 DB 425 GCATCAGACCACTTGCATCCATCAATCAAGAAACAGAGATGAACTATCACTGA 484
 QY 263 GCCAATGCTTGTAAAGGAGAGATGCTATCTCCATAGAGGAATGTCATGCAATCC 322
 DB 485 GCCAATGCTTGTAAAGGAGAGATGCTATCTCCATAGAGGAATGTCATGCAATCC 544
 QY 323 TGTAAAGGCGCTATTAAGCAAGGTCATCTTGTGCTGGGGTGGCGCTCCACATTTG 382
 DB 545 TGTAAAGGCGCTATTAAGCAAGGTCATCTTGTGCTGGGGTGGCGCTCCACATTTG 604
 QY 605 TGTAAAGGCGCGCCGATTCGATCTGTAAATAAAGCTTTTCTTATATCTCGAT 664
 DB 443 TGGCAGTGAAGAGATTTTGTGCTGTGCTGCTGCTACTGGGTGGGTAGGATC 502
 QY 665 TGGCAGTGAAGAGATTTTGTGCTGTGCTGCTGCTACTGGGTGGGTAGGATC 724
 DB 503 CGGACTGAATCCGATATTTCGTTACACCA 533
 QY 725 CGGACTGAATCCGATATTTCGTTACATTA 755

LOCUS AY255632 745 bp DNA linear VRL 30-APR-2003
DEFINITION Fowlpox virus TCP-B1en ORF201 gene, partial cds;
 Reticuloendotheliosis virus remnant LTR, complete sequence; and
 protein kinase-like protein gene, partial cds.
ACCESSION AY255632.1 GI:30267693
VERSION 1
KEYWORDS Fowlpox virus
SOURCE Fowlpox virus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.
REFERENCE 1 (bases 1 to 745)
AUTHORS Singh,P., Kim,T.-J. and Tripathy,D.N.
TITLE Re-emerging fowlpox: evaluation of isolates from vaccinated flocks
JOURNAL Avian Pathol. 29, 449-455 (2000)
REFERENCE 2 (bases 1 to 745)
AUTHORS Singh,P., Schmitzlein,W.M. and Tripathy,D.N.
TITLE Reticuloendotheliosis Virus Sequences within the Genomes of Field Strains of Fowlpox Virus Display Variability
JOURNAL J. Virol. (2003) In press
REFERENCE 3 (bases 1 to 745)
AUTHORS Singh,P., Schmitzlein,W.M. and Tripathy,D.N.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2003) Veterinary Pathobiology, University of Illinois at Urbana-Champaign, 2001 S. Lincoln Avenue, Urbana, IL 61802, USA
FEATURES
 source
 1..745
 /organism="Fowlpox virus"
 /mol_type="Genomic DNA"
 /strain="vaccine strain TCP-B1en"
 /db_xref="taxon:10261"
 /note="from CEVA Laboratory, Overland Park, KS identical to sequence in the vaccine strain 'Chick VI Pox' (Vineyard Laboratories, Vineyard, NY)"
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 /note="hypothetical protein; ORF1"
 /codon_start=1
 /evidence=not experimental
 /product="ORF201"
 /protein_id="AAP21482.1"
 /db_xref="GI:30267694"
 /translation="NNIDSLPVAVKVIYGVTVI"
 65..572
 /note="Reticuloendotheliosis virus proviral remnant LTR"
 643..>745
 /note="ORF203; ORF2"
 /codon_start=1
 /product="protein kinase-like protein"
 /protein_id="AAP21483.1"
 /db_xref="GI:30267695"
 /translation="MDIITWTMPDIQFNIDIPNIPYVDIEKPLIVISC"
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 Query Match 92.1%; Score 490.8; DB 14; Length 745;
 Best Local Similarity 99.4%; Pred. No. 5.1e-140; Mismatches 2; Indels 1; Gaps 1;
 Matches 503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 28 GAGAGAGCTCCGGGGGAGATAGCGTGGCTGCTAACTGCATATTAGCTTCTGTAATC 87
 DB 68 GAGAGAGCTCCGGGGGAGATAGCGTGGCTGCTAACTGCATATTAGCTTCTGTAATC 127
 QY 88 ATGCTTGTGCTTACCGCCGATTTGATCTTGAATATTTTCGCTGATATCAATTTCTCGGA 147
 DB 128 ATGCTTGTGCTTACCGCCGATTTGATCTTGAATATTTTCGCTGATATCAATTTCTCGGA 187
 QY 148 ATGGCATCAAGAGAGAGCTCATTAACCAATAAGGAATGTTGTGAAGCAAGATC 207
 DB 188 ATGGCATCAAGAGAGAGCTCATTAACCAATAAGGAATGTTGTGAAGCAAGATC 247
 QY 208 AGACCACTTGACCATCAATCAAGAAACAAACAGAGATGAACTATCACTGAGCCAA 267
 DB 248 AGACCACTTGACCATCAATCAAGAAACAAACAGAGATGAACTATCACTGAGCCAA 307

QY 268 TGGTGTAAAGGGGAGATGCTATCTCCAAATGAGGAAATGTCATGCAATCTCTGTAA 327
DB 308 TGGTGTAAAGGGGAGATGCTATCTCCAAATGAGGAAATGTCATGCAATCTCTGTAA 367
QY 328 GGGCTATATTAAGCCAGAGTGTCTTGGCTCGGGGTGCGCGCTCTACATATGTTGTGA 387
DB 368 GCGGCTATATTAAGCCAGAGTGTCTTGGCTCGGGGTGCGCGCTCTACATATGTTGTGA 427
QY 388 CGTGGCCCAAGATTCGATCTGTAAATAAAGCTTTTCTTCTATATCTCTAGATTTGGA 447
DB 428 CGTGGCCCAAGATTCGATCTGTAAATAAAGCTTTTCTTCTATATCTCTAGATTTGGA 487
QY 448 GTGAGAGAGATTTTGTCTGTGTGTGTGCTGCGCTACTGAGGTGAGGTGAGATTCGAC 507
DB 488 GTGAGAGAGATTTTGTCTGTGTGTGTGCTGCGCTACTGAGGTGAGGTGAGATTCGAC 547
QY 508 TGAATCGGTAGTATTTTCGTTACACA 533
DB 548 TGAAT-CGTCTAGTTCGGTACACA 572

RESULT 7
LOCUS A83548 940 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent WO9849334.
ACCESSION A83548
VERSION A83548.1 GI:6732807
KEYWORDS
SOURCE Reticuloendotheliosis virus
ORGANISM Reticuloendotheliosis virus
REFERENCE 1 (bases 1 to 940)
AUTHORS Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
TITLE Gabus-Darlix C. and Darlix J.
JOURNAL NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING SAME
Patent: WO 9849334-A 1 05-NOV-1998;
GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)
FEATURES
source
1..940
Location/Qualifiers
/organism="Reticuloendotheliosis virus"
/mol_type="unassigned DNA"
/strain="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENOMIQUE REV-A"
/db_xref="taxon:11636"

ORIGIN

Query Match 82.4%; Score 439.4; DB 6; Length 940;
Best Local Similarity 93.3%; Pred. No. 3.8e-124;
Matches 501; Conservative 0; Mismatches 11; Indels 25; Gaps 3;

QY 22 AATGTGGAGAGGAGCTTCGGGGGGAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 81
DB 1 AATGTGGAGAGGAGCTTCGGGGGGAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 60
QY 82 GTAATCATGCTTGGCTTACGCCGCAATGTAATTAATTTTGGCTGAT----- 134
DB 61 GTAATCATGCTTGGCTTACGCCGCAATGTAATTAATTTTGGCTGAT----- 120
QY 135 -----ATCATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACCAATAAG 182
DB 121 CTGGGAATCGGCATCAATTTCTGGAAATCGGCATCAAGACAGGCTCATTAACCAATAAG 180
QY 183 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGGCAATCAAGCAAAACAG 242
DB 181 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGGCAATCAAGCAAAACAG 240
QY 243 AGATGCAATCATCACTAGGCAATGTTGTTAAAGGCAATGTTATCTTCCATAGAG 302
DB 241 AGATGCAATCATCACTAGGCAATGTTGTTAAAGGCAATGTTATCTTCCATAGAG 300
QY 303 GAAATGTCATGCAACA-----TCTGTAAAGGCGCTATATAAGCAGGTGATCTTGC 357
DB 301 GAAATGTCATGCAACA-----TCTGTAAAGGCGCTATATAAGCAGGTGATCTTGC 360

QY 358 TCGGGGTGCGCGTCTACATTTGTTGTACGTGCGGCCCAAGATTCGAATCTGTAAATAA 417
DB 361 TCGGGGTGCGCGTCTACATTTGTTGTACGTGCGGCCCAAGATTCGAATCTGTAAATAA 420
QY 418 AG-CTTTTCTTCTATATCTCTAGATTTGAGAGAGGAGATTTTGTTCGTGCTTTGG 476
DB 421 AGTTTCTTCTTCTATATCTCTAGATTTGAGAGAGGAGATTTTGTTCGTGCTTTGG 480
QY 477 CTGGCTACTAGGTGGGTGAGGATTCGGAATCGGAATTCGTATTTCCGTACACA 533
DB 481 CTGGCTACTAGGTGGGTGAGGATTCGGAATTCGTATTTCCGTACACA 537

RESULT 8
LOCUS BD006232 940 bp RNA linear PAT 31-JAN-2002
DEFINITION Novel internal ribosome entry site and vector containing same.
ACCESSION BD006232
VERSION BD006232.1 GI:18634603
KEYWORDS
SOURCE Reticuloendotheliosis virus
ORGANISM Reticuloendotheliosis virus
REFERENCE 1 (bases 1 to 940)
AUTHORS Lastre,M.L., Darlix,C.G. and Darlix,J.L.
TITLE Novel internal ribosome entry site and vector containing same
JOURNAL Patent: JP 2001500021-A 1 09-JAN-2001;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
OS Reticuloendotheliosis virus
PN JP 2001500021-A/1
PD 09-JAN-2001
PF 28-APR-1998 JP 1998546672
PR 28-APR-1997 FR 97/05203
PI MARCELO LOPEZ LASTRE, CAROLINE GABUS DARLIX, JEAN LUC DARLIX PC
C12N15/86,C12N15/11//C12N15/67
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
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Location/Qualifiers
/organism="Reticuloendotheliosis virus".
/mol_type="genomic RNA"
/db_xref="taxon:11636"

FEATURES

source
1..940
Location/Qualifiers
/organism="Reticuloendotheliosis virus"
/mol_type="genomic RNA"
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ORIGIN

Query Match 82.4%; Score 439.4; DB 6; Length 940;
Best Local Similarity 93.3%; Pred. No. 3.8e-124;
Matches 501; Conservative 0; Mismatches 11; Indels 25; Gaps 3;

QY 22 AATGTGGAGAGGAGCTTCGGGGGGAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 81
DB 1 AATGTGGAGAGGAGCTTCGGGGGGAATAGCGCTGCTCGCTAATGCAATTTAGCTTCT 60
QY 82 GTAATCATGCTTGGCTTACGCCGCAATGTAATTAATTTTGGCTGAT----- 134
DB 61 GTAATCATGCTTGGCTTACGCCGCAATGTAATTAATTTTGGCTGAT----- 120
QY 135 -----ATCATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACCAATAAG 182
DB 121 CTGGGAATCGGCATCAATTTCTGGAAATCGGCATCAAGACAGGCTCATTAACCAATAAG 180
QY 183 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGGCAATCAAGCAAAACAG 242
DB 181 GAAATGTTTGTGAAGGCAAGCATCAAGCACTTGGCAATCAAGCAAAACAG 240
QY 243 AGATGCAATCATCACTAGGCAATGTTGTTAAAGGCAATGTTATCTTCCATAGAG 302
DB 241 AGATGCAATCATCACTAGGCAATGTTGTTAAAGGCAATGTTATCTTCCATAGAG 300
QY 303 GAAATGTCATGCAACA-----TCTGTAAAGGCGCTATATAAGCAGGTGATCTTGC 357


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Db      301 GAAATGTCAATGCAACATCTGTCCTGTAGCGCTATATAGCAGGTGCATCTTGC 360
Qy      358 TCGGGGTCGCGCTCCATACATATGTTGTACGTCGCGCCAGATTCGAATCTGTAATAA 417
Db      361 TCGGGGTCGCGCTCCATACATATGTTGTACGTCGCGCCAGATTCGAATCTGTAATAA 420
Qy      418 AG-CTTTTCTTCTATATCTCTCAGATTGACAGTAGAGAGATTGTCGTGTGG 476
Db      421 AGTTTTTTCTTCTATATCTCTCAGATTGACAGTAGAGAGATTGTCGTGTGG 480
Qy      477 CTGGCTACTGAGTGGGTAGGAGATCCGACTGAATCCGATGATTTTGGTACACA 533
Db      481 CTGGCTACTGAGTGGGTAGGAGATCCGACTGAATCCGATGATTTTGGTACACA 537

RESULT 9
LOCUS   S70398          545 bp      RNA      linear      VRL 23-SBP-1994
DEFINITION [LTR, U3, R and U5 regions, long terminal repeats, provirus]
           [reticuloendotheliosis virus A REV-A, A, genomic RNA, 545 nt].
ACCESSION S70398
VERSION   S70398.1 GI:547134
KEYWORDS  Reticuloendotheliosis virus
SOURCE    Reticuloendotheliosis virus
ORGANISM  Reticuloendotheliosis virus
REFERENCE 1 (bases 1 to 545)
AUTHORS   Filardo, E.J., Lee, M.F. and Humphries, E.H.
TITLE     Structural genes, not the LTRs, are the primary determinants of
           reticuloendotheliosis virus A-induced runting and bursal atrophy
           virology 202 (1), 116-128 (1994)
JOURNAL   94279132
MEDLINE   8009826
PUBMED    Genbank staff at the National Library of Medicine created this
           entry [NCBI gi548190] from the original journal article.
REMARK    This sequence comes from Fig. 3.
           Location/Qualifiers
FEATURES
   source          1..545
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                   /mol_type="genomic RNA"
                   /db_xref="taxon:11636"

ORIGIN
Query Match      82.3%; Score 438.4; DB 14; Length 545;
Best Local Similarity 93.1%; Pred. No. 7.6e-124; Indels 26; Gaps 3;
Matches 501; Conservative 0; Mismatches 11;

Qy      22 AATGTGGAGAGAGCTCCGGGGGAATAGAGCTGCTCGCTAATCTGCATATTAGTTCT 81
Db      1 AATGTGGAGAGAGCTCCGGGGGAATAGAGCTGCTCGCTAATCTGCATATTAGTTCT 60
Qy      82 GTAATCATGCTTGCCTTACCGCCCATTTGATATATTTGGCTGAT----- 134
Db      61 GTAATCATGCTTGCCTTACCGCCCATTTGATATATTTGGCTGATCATTT 120
Qy      135 -----ATCATTTCTCGGAATCGGATCAAGAGAGCTGCTAATTAACCTAAAG 182
Db      121 CTGGGAATCGGATCATTTCTCGGAATCGGATCAAGAGAGCTGCTAATTAAG 180
Qy      183 GAAATGTTTGTGAAGGACAGATCAGACATCTGCACATCCATACAGAAACAAACAG 242
Db      181 GAAATGTTTGTGAAGGACAGATCAGACATCTGCACATCCATACAGAAACAAACAG 240
Qy      243 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATAGG 302
Db      241 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATAGG 300
Qy      303 GAAATGTCAATGAAAC-----TCCTGTAAAGGCTATATTAAGCAGATGCTCTTGC 357
Db      301 GAAATGTCAATGAAACCTCTCTGTGTAAAGGCTATATTAAGCAGATGCTCTTGC 360
Qy      358 TCGGGGTCGCGCTCCATACATATGTTGTACGTCGCGCCAGATTCGAATCTGTAATAA 417

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Db      361 TCGGGGTCGCGCTCCATACATATGTTGTACGTCGCGCCAGATTCGAATCTGTAATAA 420
Qy      418 AG-CTTTTCTTCTATATCTCTCAGATTGACAGTAGAGAGATTGTCGTGTGG 475
Db      421 AGTTTTTTCTTCTATATCTCTCAGATTGACAGTAGAGAGATTGTCGTGTGG 480
Qy      476 GCTGGCTACTGAGTGGGTAGGAGATCCGACTGAATCCGATGATTTTGGTACACA 533
Db      481 GCTGGCTACTGAGTGGGTAGGAGATCCGACTGAATCCGATGATTTTGGTACACA 538

RESULT 10
LOCUS   S79845/c      583 bp      DNA      linear      VRL 07-MAY-1993
DEFINITION [REV LTR] [Marek disease virus, attenuated strain JM-H13,
           reticuloendotheliosis virus insertion, insertion, 583 nt].
ACCESSION S79845
VERSION   S79845.1 GI:244514
KEYWORDS  Gallid herpesvirus 2
SOURCE    Gallid herpesvirus 2
ORGANISM  Gallid herpesvirus 2
REFERENCE 1 (bases 1 to 583)
AUTHORS   Iefort, R., Jones, D., Kost, R., Witter, R. and Kung, H.J.
TITLE     Retrovirus insertion into herpesvirus in vitro and in vivo
           Proc. Natl. Acad. Sci. U.S.A. 89 (3), 991-995 (1992)
JOURNAL   92141243
MEDLINE   1310544
PUBMED    Genbank staff at the National Library of Medicine created this
           entry [NCBI gi548190] from the original journal article.
REMARK    This sequence comes from Fig 1C.
           Location/Qualifiers
FEATURES
   source          1..583
                   /organism="Gallid herpesvirus 2"
                   /insertion_seq="1"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:10390"

ORIGIN
Query Match      80.5%; Score 429; DB 14; Length 583;
Best Local Similarity 93.1%; Pred. No. 6.1e-121; Indels 26; Gaps 4;
Matches 501; Conservative 0; Mismatches 11;

Qy      22 AATGTGGAGAGAGCTCCGGGGGAATAGAGCTGCTCGCTAATCTGCATATTAGTTCT 81
Db      563 AATGTGGAGAGAGCTCCGGGGGAATAGAGCTGCTCGCTAATCTGCATATTAGTTCT 504
Qy      82 GTAATCATGCTTGCCTTACCGCCCATTTGATATATTTGGCTGAT----- 134
Db      503 GTAATCATGCTTGCCTTACCGCCCATTTGATATATTTGGCTGATATCATTT 444
Qy      135 -----ATCATTTCTCGGAATCGGATCAAGAGAGCTGCTAATTAACCTAAAG 182
Db      443 CTGGGAATCGGATCATTTCTCGGAATCGGATCAAGAGAGCTGCTAATTAAG 384
Qy      183 GAAATGTTTGTGAAGGACAGATCAGACATCTGCACATCCATACAGAAACAAACAG 242
Db      383 GAAATGTTTGTGAAGGACAGATCAGACATCTGCACATCCATACAGAAACAAACAG 324
Qy      243 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATAGG 302
Db      323 AGATCGAATCATATCTGAGCCAAATGTTGTAAAGGAGAGATCTATCTCAATAGG 264
Qy      303 GAAATGTCAATGAAAC-----TCCTGTAAAGGCTATATTAAGCAGATGCTCTTGC 357
Db      263 GAAATGTCAATGAAACCTCTCTGTGTAAAGGCTATATTAAGCAGATGCTCTTGC 204
Qy      358 TCGGGGTCGCGCTCCATACATATGTTGTACGTCGCGCCAGATTCGAATCTGTAATAA 417
Db      203 TCGGGGTCGCGCTCCATACATATGTTGTACGTCGCGCCAGATTCGAATCTGTAATAA 144

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QY 418 ACCTTTT-CCTCTATATCTCAGATTGCACTGAGAGAGA-ITTTGTTCTGTGTTG 475
DB 143 ATTTTTCCTCTCTATATCTCAGATTGCACTGAGAGAGA-ITTTGTTCTGTGTTG 84
QY 476 GCTGCTCTACCTGGGCTGAGGATCCGACCTGAATCCGATATTCGATCAACA 533
DB 83 GCTGCTCTACCTGGGCTGAGGATCCGACCTGAATCCGATATTCGATCAACA 26

RESULT 11
REXX2 859 bp DNA linear VRL 06-APR-1993
LOCUS Spleen necrosis virus (3' end) integrated in chicken cell.
DEFINITION V01205 J02389
ACCESSION V01205.1 GI:61794
VERSION
KEYWORDS
SOURCE Spleen necrosis virus
ORGANISM Spleen necrosis virus
Virus; Retrovirus; Retroviridae; Mammalian type C
retroviruses; 1-Mammalian type C virus group.
REFERENCE 1 (bases 1 to 859)
AUTHORS Shimotohno, K., Mizutani, S. and Temin, H.M.
TITLE Sequence of retrovirus provirus resembles that of bacterial
transposable elements
JOURNAL Nature 285 (5766), 550-554 (1980)
MEDLINE 80254544
PUBMED 6250038
FEATURES
source Location/Qualifiers
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/organism="Spleen necrosis virus"
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/db_xref="taxon:11836"
source <1..740
/organism="Spleen necrosis virus"
/proviral
/mol_type="genomic DNA"
/db_xref="taxon:11836"
741..>859
/organism="Spleen necrosis virus"
/mol_type="genomic DNA"
/db_xref="taxon:11836"
/note="cellular DNA"

ORIGIN
Query Match 58.9%; Score 313.8; DB 14; Length 859;
Best Local Similarity 85.3%; Pred. No. 2.3e-85;
Matches 424; Conservative 0; Mismatches 57; Indels 16; Gaps 6;
QY 52 GCTGCTCTACCTGGGCTGAGGATCCGACCTGAATCCGATATTCGATCAACA 111
DB 235 GCTGCTCTACCTGGGCTGAGGATCCGACCTGAATCCGATATTCGATCAACA 111
QY 112 TGTACTTGAAT--ATTTCGCTGATATCTTCGGAATCGGATCGGATCGGATCGG 168
DB 295 TGTACTTGAATGCAATTTCTCGGAATCGGATCGGATCGGATCGGATCGGATCGG 354
QY 169 ATTAACCAATTAAGGAAATGTTTGTGAAGGCAAGCATCAGACCTGCAACATCCAT 228
DB 355 ACAAACCAATTAAGGAAATGTTTGTGAAGGCAAGCATCAGACCTGCAACATCCAT 228
QY 229 CACGAACAAACGAGATCGAATCATCACT--GAGCCAAATGTTGTGAAGGCAAGTC 287
DB 415 CATTGAACGAGACGAGATCGAATCATCACT--GAGCCAAATGTTGTGAAGGCAAGTC 474
QY 288 TATCTTCAATGAGGAAATGTCATGCAATC-----CTGTAAAGCGCTATATTAAG 340
DB 475 TATCTTCAATGAGGAAATGTCATGCAATC-----CTGTAAAGCGCTATATTAAG 340
QY 341 CCAAGTGATCTCTTGTCTCGGGTCCGCTCTTACACA---TTGTTGACGTGCGGCC 397
DB 535 CCGGGTACATCTCTTGTCTCGGGTCCGCTCTTACACA---TTGTTGACGTGCGGCC 594
QY 398 AATTGCAATCTGTATTAAGCTTTTCTCTATATCTCAGATTGCACTGAGAGAGAG 457

DB 595 AGATTGCAATCTGTATTAAG--CTTTTCTCTGAAATCCAGATTCGACGATGAGAGAG 653
QY 458 ATTTTGTCTGAGTGTGCTGAGCTTACTGGTGGG--GTAGGGATCCGACATCCATCCGT 516
DB 654 ATTTTGTCTGAGTGTGCTGAGCTTACTGGTGGG--GTAGGGATCCGACATCCATCCGT 713
QY 517 AGTATTCGATCAACA 533
DB 714 AGTATTCGATCAACA 730

RESULT 12
REXX2 891 bp DNA linear VRL 29-APR-2000
LOCUS Spleen necrosis virus (5' end) integrated in chicken cell.
DEFINITION V01204 J02388 M12296
ACCESSION V01204.1 GI:61793
VERSION
KEYWORDS
SOURCE Spleen necrosis virus
ORGANISM Spleen necrosis virus
Virus; Retrovirus; Retroviridae; Mammalian type C
retroviruses; 1-Mammalian type C virus group.
REFERENCE 1 (bases 1 to 891)
AUTHORS Shimotohno, K., Mizutani, S. and Temin, H.M.
TITLE Sequence of retrovirus provirus resembles that of bacterial
transposable elements
JOURNAL Nature 285 (5766), 550-554 (1980)
MEDLINE 80254544
PUBMED 6250038
FEATURES
source Location/Qualifiers
1..891
/organism="Spleen necrosis virus"
/proviral
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/mol_type="genomic DNA"
/db_xref="taxon:9036"
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/mol_type="genomic DNA"
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ORIGIN
Query Match 58.9%; Score 313.8; DB 14; Length 891;
Best Local Similarity 85.3%; Pred. No. 2.3e-85;
Matches 424; Conservative 0; Mismatches 57; Indels 16; Gaps 6;
QY 52 GCTGCTCTACCTGGGCTGAGGATCCGACCTGAATCCGATATTCGATCAACA 111
DB 99 GCTGCTCTACCTGGGCTGAGGATCCGACCTGAATCCGATATTCGATCAACA 158
QY 112 TGTACTTGAAT--ATTTCGCTGATATCTTCGGAATCGGATCGGATCGGATCGG 168
DB 159 TGTACTTGAATGCAATTTCTCGGAATCGGATCGGATCGGATCGGATCGGATCGG 218
QY 169 ATTAACCAATTAAGGAAATGTTTGTGAAGGCAAGCATCAGACCTGCAACATCCAT 228
DB 219 ACAAACCAATTAAGGAAATGTTTGTGAAGGCAAGCATCAGACCTGCAACATCCAT 228
QY 229 CACGAACAAACGAGATCGAATCATCACT--GAGCCAAATGTTGTGAAGGCAAGTC 287
DB 279 CATTGAACGAGACGAGATCGAATCATCACT--GAGCCAAATGTTGTGAAGGCAAGTC 338
QY 288 TATCTTCAATGAGGAAATGTCATGCAATC-----CTGTAAAGCGCTATATTAAG 340
DB 339 TATCTTCAATGAGGAAATGTCATGCAATC-----CTGTAAAGCGCTATATTAAG 398
QY 341 CCAAGTGATCTCTTGTCTCGGGTCCGCTCTTACACA---TTGTTGACGTGCGGCC 397

Db 399 CCGGATCATCTCTGCTCGGGGTGCGCGTCTGACATTTGTTGTGAAGTGGCCGCC 458
 QY 398 AGATGGAATCTGTAAATAAAGCTTTTCTTCTATATCTCAGATTGGACGTGAGAG 457
 Db 459 AGATTGGAATCTGTAAATAA-CTTTTCTTCTGAAATCTCAGATTGGACGTGAGAG 517
 QY 458 ATTTTGTCTGTGTTGTGCTGCGCTTCTGAGTGGG-CTAGGAGATCCGACTGAATCCGT 516
 Db 518 ATTTTGTCTGTGTTGTGCTGCGCTTCTGAGTGGG-CTAGGAGATCCGACTGAATCCGT 577
 QY 517 AGATTTCGCTACACA 533
 Db 578 AGTACTTCGCTACACA 594

RESULT 13
 AF006066 1022 bp DNA linear VRL 16-SEP-1997
 LOCUS Fowlpox virus S envelope glycoprotein (env) gene, partial cds and
 DEFINITION 3' long terminal repeat, complete sequence.
 ACCESSION AF006066 GI:2393896
 VERSION AF006066.1 GI:2393896
 KEYWORDS Fowlpox virus
 SOURCE Fowlpox virus
 ORGANISM Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

REFERENCE 1 (bases 1 to 1022)
 AUTHORS Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
 TITLE Field and vaccine strains of fowlpox virus carry integrated
 JOURNAL sequences from the avian retrovirus, reticuloendotheliosis virus
 MEDLINE virology 235 (2), 367-376 (1997)
 PUBMED 97428585
 REFERENCE 2 (bases 1 to 1022)
 AUTHORS Hertig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.B.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAY-1997) Division of Animal Health, CSIRO, 5
 Portarlington Road, Geelong, Victoria 3213, Australia
 FEATURES location/Qualifiers

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 /organism="Fowlpox virus"
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 /strain="S (Standard Vaccine strain)"
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 /note="Standard vaccine strain from Cyanamid-Webster Pty
 Ltd, Castle Hill, New South Wales, Australia
 integrated reticuloendotheliosis virus"
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 /protein_id="AAC58241.1"
 /db_xref="GI:2393897"
 /translation="NRGGLDPLTAAOGGLALOEKCCPYANKSGIVRDKRLQENTL
 IAKRALYDNPILNGLNGFLPYLLPLGLPLFGLILFLTLTLPCKISKLTRITHAKSGS
 KNSIQSPAVQADPNRDGYPRSMI"
 409..679
 /note="3' LTR of reticuloendotheliosis provirus; LTR has
 deletions in U3, R, U5 regions; first 23 bp of U3 have
 been duplicated."
 750..>1022

CDS

ORIGIN

Query Match 38.7%; Score 206.4; DB 14; Length 1022;
 Best Local Similarity 99.1%; Pred. No.3.3e-52;
 Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TGTGGAGGAGAGCTCCGGGGGATGTGGGAGGAGCTCCGGGGGGAATAGCGTGGCTCG 60
 Db 409 TGTGGAGGAGAGCTCC-GGGGAATGTGGGAGGAGCTCCGGGGGGAATAGCGTGGCTCG 467
 QY 61 CTAACTGCCATATTAGCTTCTGATATCATGCTGCTTGCCTTAGCCGCATTGTAATTGA 120
 Db 468 CTAACTGCCATATTAGCTTCTGATATCATGCTTGTGCTTGCCTTAGCCGCATTGTAATTGA 527
 QY 121 TATATTCGCTGATATCATATTTCTGAAATCGGATCAAGAGAGGCTCATATAA 180
 Db 528 TATATTCGCTGATATCATATTTCTGAAATCGGATCAAGAGAGGCTCATATAA 587
 QY 181 AGGAATGTTTGTGTAAGGACATCAGACCTTGAC 220
 Db 588 AGGAATGTTTGTGTAAGGACATCAGACCTTGAC 627

RESULT 14
 AY255633 485 bp DNA linear VRL 30-APR-2003
 LOCUS Fowlpox virus 'Chick-n-Pox' ORF201 gene, partial cds;
 DEFINITION Reticuloendotheliosis virus remnant LTR, complete sequence; and
 ACCESSION AY255633
 VERSION AY255633.1 GI:30267696
 KEYWORDS Fowlpox virus
 SOURCE Fowlpox virus
 ORGANISM Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

REFERENCE 1 (bases 1 to 485)
 AUTHORS Singh,P., Kim,T.-U. and Tripathy,D.N.
 TITLE Re-emerging fowlpox: evaluation of isolates from vaccinated flocks
 JOURNAL Avian Pathol. 29, 449-455 (2000)
 REFERENCE 2 (bases 1 to 485)
 AUTHORS Singh,P., Schmitzlein,W.M. and Tripathy,D.N.
 TITLE Reticuloendotheliosis Virus Sequences within the Genomes of Field
 JOURNAL Strains of Fowlpox Virus Display Variability
 MEDLINE J. Virol. (2003) In press
 PUBMED 12404851
 REFERENCE 3 (bases 1 to 485)
 AUTHORS Singh,P., Schmitzlein,W.M. and Tripathy,D.N.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAR-2003) Veterinary Pathobiology, University of
 Illinois at Urbana-Champaign, 2001 S. Lincoln Avenue, Urbana, IL
 61802, USA
 FEATURES location/Qualifiers

1.485
 /organism="Fowlpox virus"
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 /strain="vaccine strain 'Chick-n-Pox'"
 /db_xref="taxon:10261"
 /note="from Fort Dodge Animal Health, Fort Dodge, IA
 identical sequence also found in strains pp-VAC (Intervet,
 Inc., Millsboro, DE), Fowlpox (Mallinckrodt Veterinary,
 Inc., Millsboro, DE), Pigeonpox (Intervet, Inc., Millsboro, DE),
 vaccines for fowlpox from Schering-Plough Animal Health,
 Omaha, NE and Select Laboratories, Gainesville, GA"
 <1.60
 /note="hypothetical protein; ORF1"
 /codon_start=1
 /evidence="not experimental"
 /product="ORF201"
 /protein_id="AAP21484.1"
 /db_xref="GI:30267697"
 /translation="NNDTSLPVAVKYIGTVIT"
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 /note="Reticuloendotheliosis virus proviral remnant LTR"
 383..>485

CDS

CDS

misc_feature
 383..>485

/note="ORF203; ORF2"
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/protein_id="AAP1485.1"
/db_xref="GI:30267698"
/translation="MDITNTMTFDIQENDIPNIPYDIEKPLVYSC"

Query Match 36.2%; Score 193; DB 14; Length 485;
Best Local Similarity 100.0%; Pred. No. 4,3e-48;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAATGCGCATATTAGCTTCTGTATC 87
DB 68 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAATGCGCATATTAGCTTCTGTATC 127
QY 88 ATGCTTGCTTGCTTACCGCCCATTTGATCTGATATATTTGCTGATATCTTCGGA 147
DB 128 ATGCTTGCTTGCTTACCGCCCATTTGATCTGATATATTTGCTGATATCTTCGGA 187
QY 148 ATGCGCATCAAGAGCGCTCATTAACCAATAAAGAAATGTTGTTGAAGCAAGCATC 207
DB 188 ATGCGCATCAAGAGCGCTCATTAACCAATAAAGAAATGTTGTTGAAGCAAGCATC 247
QY 208 AGACCACTTGAC 220
DB 248 AGACCACTTGAC 260

ORIGIN

Query Match 36.2%; Score 193; DB 14; Length 2640;
Best Local Similarity 100.0%; Pred. No. 4,7e-48;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAATGCGCATATTAGCTTCTGTATC 87
DB 908 GGAGGAGCTCCGGGGGGAATAGCGCTGCTCGCTAATGCGCATATTAGCTTCTGTATC 967
QY 88 ATGCTTGCTTGCTTACCGCCCATTTGATCTGATATATTTGCTGATATCTTCGGA 147
DB 968 ATGCTTGCTTGCTTACCGCCCATTTGATCTGATATATTTGCTGATATCTTCGGA 1027
QY 148 ATGCGCATCAAGAGCGCTCATTAACCAATAAAGAAATGTTGTTGAAGCAAGCATC 207
DB 1028 ATGCGCATCAAGAGCGCTCATTAACCAATAAAGAAATGTTGTTGAAGCAAGCATC 1087
QY 208 AGACCACTTGAC 220
DB 1088 AGACCACTTGAC 1100

Search completed: May 25, 2004, 02:09:40
Job time : 2254 secs

FEATURES

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1. .2640
/organism="Fowlpox virus"
/mol_type="genomic DNA"
/strain="M (mild vaccine strain)"
/db_xref="taxon:10261"
/note="mild vaccine strain from Cyanamid-Webster Pty Ltd, Castle Hill, New South Wales, Australia.
Part 1 A' fragment
integrated reticuloendotheliosis virus"
49. .900
/note="ORF1"
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LDNRCKLPMPLIPLSKYDFTFTDLSVLSKSNVKTLSKATSMKSYNNDTSLPVAVKY
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905. .1152
/note="remnant of LTR of reticuloendotheliosis virus"
1223. .2080
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/protein_id="AAC58236.1"
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VLKISGAYNTYKRVNFMVAPDYMLMDISNTYIKSEIRPGLVITWEITRKLPS
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 00:25:56 ; Search time 351 Seconds
(without alignments)
6450.967 Million cell updates/sec

Title: US-10-623-891-2

Perfect score: 533

Sequence: 1 tctggggagggagctccggggg.....cgtgattcttcggtacacaa 533

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506.8	95.1	512	2	AAx26109
2	506	94.9	536	2	AAx26110
3	506	94.9	4643	2	AAx26113
4	439.4	82.4	940	2	AAV63778
5	206.4	38.7	296	2	AAx26111
6	206.4	38.7	1022	2	AAx26115
7	193	36.2	298	2	AAx26112
8	193	36.2	1100	2	AAx26114
9	193	36.2	266145	9	ADe87477
10	155	29.1	578	2	AAV63779
11	145	27.2	3878	2	AAQ76041
12	145	27.2	5528	2	AAQ76038
13	134.6	25.3	5525	2	AAQ76039
14	127.6	23.9	5519	2	AAQ76040
15	33.8	6.3	714	4	AAK93188
16	33.8	6.3	714	4	AAK93188
17	33.8	6.3	2604	5	AAK94345
18	33.8	6.3	13079	5	ABAI6338
19	33.8	6.3	25967	5	ABAI6339
20	33.8	6.3	96960	7	ADCF62734
21	33.8	6.3	96960	7	ADCF62734
22	33.8	6.3	96960	9	ADB87938
23	33.8	6.3	96960	9	ADB87938

24	33.8	6.3	96960	9	ADB92112	AdB92112 Human MDR
25	33.8	6.3	123785	7	ABX77171	ABX77171 DNA seque
26	33.8	6.3	2000	7	ADAX71938	AdA71938 Rice gene
27	33.4	6.3	3824	9	ADBE3200	AdE63200 Human gen
28	33.4	6.3	3824	9	ADBE3196	AdE63196 Human gen
29	33.4	6.3	3824	9	ADBE3208	AdE63204 Human gen
30	33.4	6.3	3824	9	ADBE3204	AdE63204 Human gen
31	33.4	6.3	6617	4	AAI97964	AAI97964 Lawsonia
32	33.4	6.3	6617	8	ACA92322	ACA92322 Lawsonia
33	33.2	6.2	2000	7	ADA71938	AdA71938 Rice gene
34	33	6.2	557	6	ABN61561	ABN61561 Human can
35	33	6.2	4703	3	AACT6621	AACT6621 Human ORF
36	33	6.2	110000	2	AAV21209	AAV21209 07 of
37	32.6	6.1	96595	8	ADA02726	ADA02726 Human SYK
38	32.6	6.1	96595	9	ADA02726	ADA02726 Human SYK
39	32.2	6.0	703	4	AAK92046	AAK92046 Human CDN
40	32.2	6.0	703	4	AAK93694	AAK93694 Human CDN
41	32.2	6.0	3388	7	AAAD47154	AAK47154 Human nuc
42	32.2	6.0	3396	4	AAK94808	AAK94808 Human ful
43	32.2	6.0	3410	7	ABX70998	ABX70998 Novel hum
44	32.2	6.0	20346	8	ADB66951	ADB66951 E. coli K
45	32	6.0	9347	6	ABL49336	ABL49336 Human pol

ALIGNMENTS

RESULT 1
AAx26109 standard; DNA; 512 BP.
AC AAX26109;
XX 17-OCT-2003 (revised)
DT 20-MAY-1999 (first entry)
XX
DE Chicken syncytial virus provirus REV LTR sequence.
XX
KM Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
KM vaccine; chicken; LTR; long terminal repeat; ss.
XX
OS Reticuloendotheliosis virus.
XX
SS WO9907852-A1.
XX
PD 18-FEB-1999.
XX
PF 07-AUG-1998; 98MO-AU000628.
XX
PR 08-AUG-1997; 97AU-00008454.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Hertig C, Coupar BEH, Gould AR, Boyle DB;
XX WPI; 1999-167428/14.
XX
DR Recombinant vaccine against fowlpox virus - is free of contamination from
XX reticuloendotheliosis virus, used to prevent the virus occurrence in
XX chickens.
XX
PS Example 4; Fig 5; 127pp; English.
XX
XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
XX acid does not encode an active reticuloendotheliosis virus (REV), and
XX whose genome does not contain any REV sequence. The recombinant FPV is
XX used to produce a vaccine against fowlpox virus. The vaccine is used to
XX prevent the occurrence of fowlpox virus in chickens. The chickens can be
XX vaccinated at older than 1 day of age. Alternatively, chickens older than
XX 1 day can be vaccinated with the vaccine subsequent to vaccination with
XX FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
XX of FPV carry integrated REV sequences. Some of the FPV strains carry a
XX near full length provirus of REV, and can give rise to infectious REV

CC when transfect into cell cultures and when chickens are infected. The
CC present invention provides the means by which a FPV vaccine free from
CC contamination by REV may be produced. (Updated on 17-OCT-2003 to
CC standardise OS field)

Sequence 512 BP; 130 A; 113 C; 129 G; 140 T; 0 U; 0 Other;

Query Match	95.1%;	Score 506.8;	DB 2;	Length 512;
Best Local Similarity	99.6%;	Pred. No. 8.7e-162;		
Matches 508; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	24	TGTGGAGGGAGCTCCGGGGGAAATACGCTGGCTCGTAACTGGCAATTAAGCTTCGT	83
Db	1	TGTGGAGGGAGCTCCGGGGGAAATACGCTGGCTCGTAACTGGCAATTAAGCTTCGT	60
QY	84	AATCATGCTTGCTTGCTTATGCCGCATATGTACTGATATATTTGCTGATATCATTTCT	143
Db	61	AATCATGCTTGCTTGCTTATGCCGCATATGTACTGATATATTTGCTGATATCATTTCT	120
QY	144	CGGATCGGCAATCAAGACAGGCTCATTAACATATAAAGGAAATGTTTGTAAGGGCAG	203
Db	121	CGGATCGGCAATCAAGACAGGCTCATTAACATATAAAGGAAATGTTTGTAAGGGCAG	180
QY	204	CATCAGACCATTCGACCAATCCAAATCAGAACAAACAGAGTCGACATATCATCTAG	263
Db	181	CATCAGACCATTCGACCAATCCAAATCAGAACAAACAGAGTCGACATATCATCTAG	240
QY	264	CCAATGCTTGAAGGCGAGATGCTATCTCCAAATGAGGGGAAATGTCATGACATCTT	323
Db	241	CCAATGCTTGAAGGCGAGATGCTATCTCCAAATGAGGGGAAATGTCATGACATCTT	300
QY	324	GTAAGCGGCTATATTAAGCCAGGTGATCTTCTTCGCGGATCGCGTCTTACATATGT	383
Db	301	GTAAGCGGCTATATTAAGCCAGGTGATCTTCTTCGCGGATCGCGTCTTACATATGT	360
QY	384	GTCAGCGGCGCCCAATCGAATCTGTATATAAGCTTTTCTTATATCTTCAGATT	443
Db	361	GTCAGCGGCGCCCAATCGAATCTGTATATAAGCTTTTCTTATATCTTCAGATT	420
QY	444	GCGAGTAGAGAGATTTTGTTCGTGTGTTGGCTGCGCTTCTGAGTGGGGTAGGGAATC	503
Db	421	GCGAGTAGAGAGATTTTGTTCGTGTGTTGGCTGCGCTTCTGAGTGGGGTAGGGAATC	480
QY	504	GGAAGTAATCCGATGATTTCCGTACACA	533
Db	481	GGAAGTAATCCGATGATTTCCGTACACA	510

RESULT 2	
AAX26110	
ID	AAX26110 standard; DNA; 536 BP
vv	

AC	AA26110;	
XX		
DT	20-MAY-1999	(first entry)
XX		
DE	Fowlpox virus (FPV M5)	LTR sequence.
XX		
KW	Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV,	
KM	vaccine; chicken; LTR; long terminal repeat; ss.	
XX		
OS	Fowlpox virus.	
XX		
PN	MO9907852-A1.	
XX		
PD	18-FEB-1999.	
XX		
PF	07-AUG-1998;	98MO-AU000628.
XX		
PR	08-AUG-1997;	97AU-00008454.
XX		
PA	(CSIR)	COMMONWEALTH SCI & IND RES ORG.
XX		

PI Hertig C, Coupar BEH, Gould AR, Boyle DB;
 XX
 XX
 DR WPI; 1999-167428/14.
 XX
 PT Recombinant vaccine against fowlpox virus - is free of contamination from
 PT reiculoetheliosis virus, used to prevent the virus occurrence in
 PT chickens.

PS Claim 18; Fig 5; 127pp; English.
 YY

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
CC acid does not encode an active reticuloendotheliosis virus (REV), and
CC whose genome does not contain any REV sequence. The recombinant FPV is
CC used to produce a vaccine against fowlpox virus. The vaccine is used to
CC prevent the occurrence of fowlpox virus in chickens. The chickens can be
CC vaccinated at older than 1 day of age. Alternatively, chickens older than
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
CC near full length provirus of REV, and can give rise to infectious REV
CC when transacted into cell cultures and when chickens are infected. The
CC present invention provides the means by which a FPV vaccine free from
CC contamination by REV may be produced. Sequences AXX26110-115 represent
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
CC molecule can comprise a FPV LTR sequence selected from the above
SQ
XQ Sequence 536 BP; 145 A; 115 C; 133G; 143 T; 0 U; 0 Other;

Query Match 94.9%; Score 506; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 506; Conservative 0; Mismatches 0; Gaps 0

Qy	28	GGAGGAGCTCGGGGGGAAATGACCTGGCTGCTAACTGCAATATTAAGCTTCTGTAATC	87
Db	29	GGAGGGAGCTCGGGGGGAAATGACCTGGCTGCTAACTGCAATATTAAGCTTCTGTAATC	88
Qy	88	ATGCTTTCCTGCTTACCGCCATTGTGACTTGATATATTTGGCTGATATCATATTTCTCGGA	147
Db	89	ATGCTTTCCTGCTTACCGCCATTGTGACTTGATATATTTGGCTGATATCATATTTCTCGGA	148
Qy	148	ATCGGCATCAAGAGAGGCTCATTAACATTAAGAAATGTTTGTGAAGCAAGATC	207
Db	149	ATCGGCATCAAGAGAGGCTCATTAACATTAAGAAATGTTTGTGAAGCAAGATC	208
Qy	208	AACACACTTGCAACATCAATCAACGAAACAAACAGAGATCGAATATCATACTAGCCAA	267
Db	209	AACACACTTGCAACATCAATCAACGAAACAAACAGAGATCGAATATCATACTAGCCAA	268
Qy	268	TGGTTGTAAAGGGGAGATGTCTATCTCTCAAGAGAGGAAAATGTATGACAACTCTGTAA	327
Db	269	TGGTTGTAAAGGGGAGATGTCTATCTCTCAAGAGAGGAAAATGTATGACAACTCTGTAA	328
Qy	328	GGGGCTATATAAGCCAGAGTGCATCTCTTGTCTCGGGGGTGCAGCTCTACACATTTGTGTA	387
Db	329	GGGGCTATATAAGCCAGAGTGCATCTCTTGTCTCGGGGGTGCAGCTCTACACATTTGTGTA	388
Qy	388	CGTGGGGCCAGATTCGAAATCTGTAAATTAAGCTTTTCTTCTATATCTCAAGTTGGCA	447
Db	389	CGTGGGGCCAGATTCGAAATCTGTAAATTAAGCTTTTCTTCTATATCTCAAGTTGGCA	448
Qy	448	GTGAGAGAGATTTTGTTCGTGTGTGTGGCTGAGCCTACTGGGTGGGGTAAAGATCCGGAC	507
Db	449	GTGAGAGAGATTTTGTTCGTGTGTGTGGCTGAGCCTACTGGGTGGGGTAAAGATCCGGAC	508
Qy	508	TGAATCCCTAGTATTTGGGTACACA	533
Db	509	TGAATCCCTAGTATTTGGGTACACA	534

RESULT 3
AAK26113
ID AAK26113 standard; DNA; 4643 BP.
XX

AC AAX26113;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Fowlpox virus (FPV S) 5' LTR sequence.
 XX
 KM Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
 KM vaccine; chicken; LTR; long terminal repeat; ss.
 XX
 OS Fowlpox virus.
 PN MO9907852-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 07-AUG-1998; 98MO-AU000628.
 XX
 PR 08-AUG-1997; 97AU-00008454.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Hertig C, Coupar BEH, Gould AR, Boyle DB;
 XX
 DR WPI; 1999-167428/14.
 XX
 PT Recombinant vaccine against fowlpox virus - is free of contamination from
 PT reticuloendotheliosis virus, used to prevent the virus occurrence in
 PT chickens.
 XX
 PS Claim 18; Fig 6; 127pp; English.
 XX
 CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
 CC acid does not encode an active reticuloendotheliosis virus (REV), and
 CC whose genome does not contain any REV sequence. The recombinant FPV is
 CC used to produce a vaccine against fowlpox virus. The vaccine is used to
 CC prevent the occurrence of fowlpox virus in chickens. The chickens can be
 CC vaccinated at older than 1 day of age. Alternatively, chickens older than
 CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
 CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
 CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
 CC near full length provirus of REV, and can give rise to infectious REV
 CC when transfected into cell cultures and when chickens are infected. The
 CC present invention provides the means by which a FPV vaccine free from
 CC contamination by REV may be produced. Sequences AAX26110-115 represent
 CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
 CC molecule can comprise a FPV LTR sequence selected from the above
 CC
 XX
 SQ Sequence 4643 BP; 1326 A; 1015 C; 1127 G; 1175 T; 0 U; 0 Other;
 XX
 Query Match 94.9%; Score 506; DB 2; Length 4643;
 Best Local Similarity 100.0%; Pred. No. 5.2e-161;
 Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 28 GGAGGAGAGCTCCGGGGGAATAGCGCTGCTGCTAACTGCATATTAAGCTTCTGTATC 87
 DB 1259 GGAGGAGAGCTCCGGGGGAATAGCGCTGCTGCTAACTGCATATTAAGCTTCTGTATC 1318
 QY 88 ATGCTTGCTTGCCTTACCGCCGATTTGATTAATTTTGGCTGATATCAATTTCTGGA 147
 DB 1319 ATGCTTGCTTGCCTTACCGCCGATTTGATTAATTTTGGCTGATATCAATTTCTGGA 1378
 QY 148 ATGGGAGTCAAGAGCAGGCTCATTAACATTAAGGAATTTTGTGAAGGCAAGATC 207
 DB 1379 ATGGGAGTCAAGAGCAGGCTCATTAACATTAAGGAATTTTGTGAAGGCAAGATC 1438
 QY 208 AGACCACTTGCACCATCAATCAAGCAAAACAGAGATGAACTATCATAGAGCAA 267
 DB 1439 AGACCACTTGCACCATCAATCAAGCAAAACAGAGATGAACTATCATAGAGCAA 1498
 QY 268 TGGTTGTAAGGGGAGATGCTATCTTCAATGAGGAAAAATGTATGCAACATCTGTAA 327
 DB 1499 TGGTTGTAAGGGGAGATGCTATCTTCAATGAGGAAAAATGTATGCAACATCTGTAA 1558

QY 328 GCGGCTATATTAAGCCAGGTGATCTTGTGCTGGGGGTGCGCTGCTAAGACATTTGTGTGA 387
 DB 1559 GCGGCTATATTAAGCCAGGTGATCTTGTGCTGGGGGTGCGCTGCTAAGACATTTGTGTGA 1618
 QY 388 CGTCCGGCCCAAGATTGGAATCTGTATTAAGGCTTTTCTTCTATATCTTCAGATTGGCA 447
 DB 1619 CGTCCGGCCCAAGATTGGAATCTGTATTAAGGCTTTTCTTCTATATCTTCAGATTGGCA 1678
 QY 448 GTGAGAGGAGATTTTGTGCTGGGTTGCTGAGCTACTAGGAGGAGTAAGGATCCGAC 507
 DB 1679 GTGAGAGGAGATTTTGTGCTGGGTTGCTGAGCTACTAGGAGGAGTAAGGATCCGAC 1738
 QY 508 TGAATCGTAGTATTTTCGTACACA 533
 DB 1739 TGAATCGTAGTATTTTCGTACACA 1764
 XX
 RESULT 4
 ID AAV63778 standard; DNA; 940 BP.
 XX
 AC AAV63778;
 XX
 DT 17-MAR-1999 (first entry)
 XX
 DE Sequence derived from the 5' end of REV-A.
 XX
 KM Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;
 KM type C retrovirus; internal ribosome entry site; IRES; encapsidation;
 KM retroviral vector; gene therapy; ss.
 XX
 OS Reticuloendotheliosis virus.
 XX
 PN FR2762615-A1.
 XX
 PD 30-OCT-1998.
 XX
 PF 28-APR-1997; 97FR-00005203.
 XX
 PR 28-APR-1997; 97FR-00005203.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Lopez Lastra M, Gabus Darlix C, Darlix JL;
 XX
 DR WPI; 1999-037487/04.
 XX
 PT Expression vectors containing IRES and/or encapsidation enhancer -
 PT derived from type C retrovirus other than FMLV and MoMLV.
 XX
 PS Claim 5; Page 31-32; 43pp; French.
 XX
 CC The present sequence is derived from the 5' end of the genomic RNA of
 CC Reticuloendotheliosis virus type A (REV-A). The specification also
 CC describes nucleotide sequence derived from all or part of the 5' end of
 CC the genomic RNA of a type C retrovirus other than Friend murine leukemia
 CC virus (FMLV) and Moloney murine leukemia virus (MoMLV). The 5' derived
 CC sequences are used as an internal ribosome entry site (IRES) in a vector
 CC for permitting or enhancing the encapsidation of a retroviral vector. The
 CC vectors can be used for gene therapy, production of recombinant
 CC polypeptides or production of transgenic animals
 CC
 XX
 SQ Sequence 940 BP; 190 A; 225 C; 260 G; 0 T; 265 U; 0 Other;
 XX
 Query Match 82.4%; Score 439.4; DB 2; Length 940;
 Best Local Similarity 68.2%; Pred. No. 1.1e-138;
 Matches 366; Conservative 135; Mismatches 11; Indels 25; Gaps 3;
 XX
 QY 22 AATGTGGAGGGAGCTCCGGGGGAATAGCGCTGCTAAGCTGCAATTAAGCTTCT 81
 DB 1 AATGTGGAGGGAGCTCCGGGGGAATAGCGCTGCTAAGCTGCAATTAAGCTTCT 60
 QY 82 GTAATCATGCTTGTGCTTACCGCCGATTTGATTAATATTTTCGTGAT----- 134

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Db      61  GUAAUACAGUCUCUGCCUACCCGCAUUGACUUGAUUUAUUUCCUUAUUCUUAUU
Qy      135  -----ATCATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACCAATTAAG
Db      121  CUUGGAUUCGGCAUUCUUUUCUGAUUCGGCAUCAAAGACAGGCUCAUAGACUAAAAG
Qy      183  GAAATGTTTGTGAAGCAAGCATCAGACCACTTGCACATCCATCCATCAGAACACACG
Db      181  GAAAUUUCUGUGGAGGCGAGCAUCAGACCAUUCGCGCAUCCAUACAAGGCAAAACACG
Qy      243  AGATGCACTATCATCTAGCAATGCTTGAAGGCGAGATCTATCTCCAAATGAG
Db      241  AGUUGACACUACUACUAGCAGCAUUGUUAAGGCGACAUUCUUAUUGGCAUUGG
Qy      303  GAAATGTCATGCAACA-----TCTTGAAGCGCTATTAAGCAGATCTCTTCG
Db      301  GAAAUUUCUACUACUACUUGUUAAGGCGCAUUAUUAAGCAGUUCUUCUUC
Qy      358  TCGGGGTGCGCGTCTTCAACATTTGTGACGTGCGGCGCAGATTCGATCTGTAATAA
Db      361  UCGGGGUCGCGGCUACAUUUGUUGAGCGCGGCCAGAUUUGAAUUCUUAUUA
Qy      418  AG-CTTTTCTTCTATATCTCAGATTGAGAGAGAGAGATTGTTGTGTGTG
Db      421  AGUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
Qy      477  CTGCGCTTACTGAGGTGGGTGAGGATCCGAGCTGATCCGATGTTTGGTGAACA
Db      481  CUGGCGUACUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG

```

RESULT 5
ID AAX26111 standard; DNA; 296 BP.
XX AAX26111;

AC AAX26111;

DT 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV S3') LTR sequence.

KM Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

XX 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB,

XX WPI, 1999-167428/14.

PT Recombinant vaccine against fowlpox virus - is free of contamination from
PT reticuloendotheliosis virus, used to prevent the virus occurrence in
PT chickens.

XX Claim 18; Fig 5; 127dp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
CC acid does not encode an active reticuloendotheliosis virus (REV), and
CC whose genome does not contain any REV sequence. The recombinant FPV is
CC used to produce a vaccine against fowlpox virus. The vaccine is used to
CC prevent the occurrence of fowlpox virus in chickens. The chickens can be
CC vaccinated at older than 1 day of age. Alternatively, chickens older than

CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
CC near full length provirus of REV, and can give rise to infectious REV
CC when transfected into cell cultures and when chickens are infected. The
CC present invention provides the means by which a FPV vaccine free from
CC contamination by REV may be produced. Sequences AAX26110-115 represent
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
CC molecule can comprise a FPV LTR sequence selected from the above

Sequence 296 BP; 75 A; 58 C; 81 G; 82 T; 0 U; 0 Other;
Query Match 38.7%; Score 206.4; DB 2; Length 296;
Best Local Similarity 99.1%; Pred. No. 1.5e-59;
Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

Qy      1  TGTGGAGGAGGCTCCGGGGAATGTGAGGAGAGCTCGGGGGGAATAGCGCTGCTCG
Db      1  TGTGGAGGAGGAGCTCC-GGGGAATGTGAGGAGAGCTCGGGGGGAATAGCGCTGCTCG
Qy      61  CTAAGTCCATATATAGCTTCTGTAATCATGCTTCTTCCCTTAAAGCCATTTGACTTGA
Db      60  CTAAGTCCATATATAGCTTCTGTAATCATGCTTCTTCCCTTAAAGCCATTTGACTTGA
Qy      121  TATATTCGCTGATATCATATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACATTA
Db      120  TATATTCGCTGATATCATATTTCTCGGAATCGGCATCAAGACAGGCTCATTAACATTA
Qy      181  AGGAATGTTTGTGAAGCAAGCATTCAGACCACTTGAC
Db      180  AGGAATGTTTGTGAAGCAAGCATTCAGACCACTTGAC

```

RESULT 6
ID AAX26115 standard; DNA; 1022 BP.
XX AAX26115;

AC AAX26115;

DT 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV S) 3' LTR sequence.

KM Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

XX 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB,

XX WPI, 1999-167428/14.

PT Recombinant vaccine against fowlpox virus - is free of contamination from
PT reticuloendotheliosis virus, used to prevent the virus occurrence in
PT chickens.

XX Claim 18; Fig 6; 127dp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic
CC acid does not encode an active reticuloendotheliosis virus (REV), and
CC whose genome does not contain any REV sequence. The recombinant FPV is
CC used to produce a vaccine against fowlpox virus. The vaccine is used to
CC prevent the occurrence of fowlpox virus in chickens. The chickens can be

CC vaccinated at older than 1 day of age. Alternatively, chickens older than
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
CC near full length provirus of REV, and can give rise to infectious REV
CC when transduced into cell cultures and when chickens are infected. The
CC present invention provides the means by which a FPV vaccine free from
CC contamination by REV may be produced. Sequences AAX26110-115 represent
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
CC molecule can comprise a FPV LTR sequence selected from the above

XX SQ Sequence 1022 BP; 315 A; 209 C; 218 G; 280 T; 0 U; 0 Other;

Query Match 38.7%; Score 206.4; DB 2; Length 1022;

Best Local Similarity 99.1%; Pred. No. 2.9e-59; Matches 218; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TGTGGAGGAGCTCCGGGGGAAATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCG 60
DB TGTGGAGGAGCTCCGGGGGAAATGTGGAGGAGCTCCGGGGGAAATAGCGCTGCTCG 467
QY 61 CTAACTGCCATATTAGCTTCTGTATCATGCTTGTGCTTACCGCCATTTGACTTGA 120
DB 468 CTAACTGCCATATTAGCTTCTGTATCATGCTTGTGCTTACCGCCATTTGACTTGA 527
QY 121 TATATTGGCGATATCATTTCTGGAAATCGGCATCAAGACAGCTCATTAACCATAAA 180
DB 528 TATATTGGCGATATCATTTCTGGAAATCGGCATCAAGACAGCTCATTAACCATAAA 587
QY 181 AGAATAATGTTTGTGAAGGAGCATGACACCACTTCAC 220
DB 588 AGAATAATGTTTGTGAAGGAGCATGACACCACTTCAC 627

RESULT 7
AAX26112

ID AAX26112 standard; DNA; 298 BP.

XX AAX26112;

AC 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV M3) LTR sequence.

DE Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;

XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

XX 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX WPI; 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from

XX PT reticuloendotheliosis virus, used to prevent the virus occurrence in

XX PT chickens.

XX Claim 18; Fig 5; 127pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic

XX acid does not encode an active reticuloendotheliosis virus (REV), and

XX whose genome does not contain any REV sequence. The recombinant FPV is

XX used to produce a vaccine against fowlpox virus. The vaccine is used to

CC prevent the occurrence of fowlpox virus in chickens. The chickens can be
CC vaccinated at older than 1 day of age. Alternatively, chickens older than
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
CC near full length provirus of REV, and can give rise to infectious REV
CC when transduced into cell cultures and when chickens are infected. The
CC present invention provides the means by which a FPV vaccine free from
CC contamination by REV may be produced. Sequences AAX26110-115 represent
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
CC molecule can comprise a FPV LTR sequence selected from the above

XX SQ Sequence 298 BP; 84 A; 59 C; 73 G; 82 T; 0 U; 0 Other;

Query Match 36.2%; Score 193; DB 2; Length 298;

Best Local Similarity 100.0%; Pred. No. 5.5e-55; Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAAGGAGCTCCGGGGGAAATAGCGCTGCTGCTAACTGCAATATTAGCTTGTATC 87
DB 29 GGAAGGAGCTCCGGGGGAAATAGCGCTGCTGCTAACTGCAATATTAGCTTGTATC 88
QY 88 ATGCTTGCTTGCCTTACCGCCCATTTGACTTGAATATTTGCTGATATCTTCGGA 147
DB 89 ATGCTTGCTTGCCTTACCGCCCATTTGACTTGAATATTTGCTGATATCTTCGGA 148
QY 148 ATGCGCATCAAGAGCGCTCATTAACCATTAAGAAATGTTTGTGAAGCAGCATC 207
DB 149 ATGCGCATCAAGAGCGCTCATTAACCATTAAGAAATGTTTGTGAAGCAGCATC 208
QY 208 AGACCACTTCAC 220
DB 209 AGACCACTTCAC 221

RESULT 8
AAX26114

ID AAX26114 standard; DNA; 1100 BP.

XX AAX26114;

AC 20-MAY-1999 (first entry)

XX Fowlpox virus (FPV M3) LTR sequence.

DE Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;

XX vaccine; chicken; LTR; long terminal repeat; ss.

OS Fowlpox virus.

XX WO9907852-A1.

XX 18-FEB-1999.

XX 07-AUG-1998; 98WO-AU000628.

XX 08-AUG-1997; 97AU-00008454.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Hertig C, Coupar BEH, Gould AR, Boyle DB;

XX WPI; 1999-167428/14.

XX Recombinant vaccine against fowlpox virus - is free of contamination from

XX PT reticuloendotheliosis virus, used to prevent the virus occurrence in

XX PT chickens.

XX Claim 18; Fig 6; 127pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) whose nucleic

XX acid does not encode an active reticuloendotheliosis virus (REV), and

XX whose genome does not contain any REV sequence. The recombinant FPV is

CC used to produce a vaccine against fowlpox virus. The vaccine is used to
CC prevent the occurrence of fowlpox virus in chickens. The vaccine can be
CC vaccinated at older than 1 day of age. Alternatively, chickens older than
CC 1 day can be vaccinated with the vaccine subsequent to vaccination with
CC FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains
CC of FPV carry integrated REV sequences. Some of the FPV strains carry a
CC when full length provirus of REV, and can give rise to infectious REV
CC present invention provides the means by which a FPV vaccine free from
CC contamination by REV may be produced. Sequences AAY26110-115 represent
CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
CC molecule can comprise a FPV LTR sequence selected from the above
SQ Sequence 1100 BP; 392 A; 177 C; 196 G; 335 T; 0 U; 0 Other;

Query Match
Best Local Similarity 36.2%; Score 193; DB 2; Length 1100;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGTGCATATTAAGTTCGTATC 87
DB 908 GGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGTGCATATTAAGTTCGTATC 87
QY 88 ATGCTTGTCTGCTTACCGCCATTTGATGATATTTGCGTATATCATTTTCGGA 147
DB 968 ATGCTTGTCTGCTTACCGCCATTTGATGATATTTGCGTATATCATTTTCGGA 147
QY 148 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207
DB 1028 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207
QY 208 AGACCACTTGAC 220
DB 1088 AGACCACTTGAC 1100

RESULT 9
ADE87477
ID ADE87477 standard; DNA; 266145 BP.
XX
AC ADE87477;
XX
DT 29-JAN-2004 (first entry)
XX
DE Fowlpox virus genome DNA.
XX
KM fowlpox virus; FPV; virulence; tuberculostatic; protozoacide; antipyrctic;
KM cytostatic; hepatotropic; antibacterial; vaccine; malaria; tuberculostatic;
KM East Coast fever; avipox virus; influenza; hepatitis;
KM human papilloma virus; tumour; leishmaniasis; listeriosis; chelaria;
KM gene; db.

OS Fowlpox virus.
XX
PN WO2003047617-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-GB005411.
XX
PR 30-NOV-2001; 2001GB-00028733.
XX
PR 30-NOV-2001; 2001US-0334649P.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Laidlaw S, Skinner M, Hill A, Gilbert S, Anderson R;
XX
DR WPI; 2003-513700/48.
XX
PT Treating and/or preventing e.g. malaria or tuberculostatic, or eliciting an
PT immune response, comprises administering a priming composition and a
PT boosting composition containing a non-replicating viral vector in either
PT order.

XX
PS Claim 30; SEQ ID NO 1; 302pp; English.
XX

CC The invention relates to a fowlpox virus (FPV) genome which has
CC modifications in one or more wild-type FPV genes. The invention further
CC relates to a novel method for treating and/or preventing a disease in a
CC subject comprising administering two compositions, each containing a non-
CC replicating viral vector. At least one of the compositions comprises a
CC fowlpox virus derived from a fowlpox virus. The novel compositions have
CC the following activities: virulence, tuberculostatic, protozoacide,
CC antipyrctic, cytostatic, hepatotropic, and antibacterial. The non-
CC replicating viral vector is useful in a vaccine for an animal,
CC particularly a mammal such as a primate, specifically human. The non-
CC or boosting composition, or the kit is useful for manufacturing a
CC medicament for treating and/or preventing a disease which is, or results
CC from, a chronic infection such as malaria, tuberculostatic or East Coast
CC fever, or for eliciting a T-cell immune response in a subject. Non-
CC cultured CEF cells are useful for growing an avipox virus, such as
CC fowlpox virus. The method or the vaccine may further be used to treat or
CC prevent influenza, hepatitis, human papilloma virus and other viral
CC infections, malignancies such as tumours, leishmaniasis, listeriosis, and
CC virus genome of the invention.

SQ Sequence 266145 BP; 92375 A; 41026 C; 40846 G; 91897 T; 0 U; 1 Other;
Query Match
Best Local Similarity 36.2%; Score 193; DB 9; Length 266145;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGTGCATATTAAGTTCGTATC 87
DB 221741 GGAGGAGCTCCGGGGGAAATAGCGTGGCTGCTAAGTGCATATTAAGTTCGTATC 87
QY 88 ATGCTTGTCTGCTTACCGCCATTTGATGATATTTGCGTATATCATTTTCGGA 147
DB 221801 ATGCTTGTCTGCTTACCGCCATTTGATGATATTTGCGTATATCATTTTCGGA 147
QY 148 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207
DB 221861 ATCGGATCAAGAGAGGCTCATTAACCATTAAGAAATGTTGTTGAAGCAAGCATC 207
QY 208 AGACCACTTGAC 220
DB 221921 AGACCACTTGAC 221933

RESULT 10
AAV63779
ID AAV63779 standard; DNA; 578 BP.
XX
AC AAV63779;
XX
DT 17-MAR-1999 (first entry)
XX
DE Sequence derived from the 5' end of REV-A.
XX
KM Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;
KM type C retrovirus; internal ribosome entry site; IRBS; encapsidation;
KM retroviral vector; gene therapy; ss.
XX
OS Reticuloendotheliosis virus.
XX
PN FR2762615-A1.
XX
PD 30-OCT-1998.
XX
PF 28-APR-1997; 97FR-00005203.
XX
PR 28-APR-1997; 97FR-00005203.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX

PI Lopez Lastrea M, Gabus Darlix C, Darlix JL;
XX MPI, 1999-037487/04.
XX
XX
XX Expression vectors containing IRES and/or encapsidation enhancer -
PT derived from type C retrovirus other than FMLV and MoMLV.
XX
XX
PS Claim 6; Page 32; 43pp; French.
XX
XX The present sequence is derived from the 5' end of the genomic RNA of
CC Reticuloendotheliosis virus type A (REV-A). The specification also
CC describes nucleotide sequence derived from all or part of the 5' end of
CC the genomic RNA of a type C retrovirus other than Friend murine leukaemia
CC virus (FMLV) and Moloney murine leukaemia virus (MoMLV). The 5' derived
CC sequences are used as an internal ribosome entry site (IRES) in a vector
CC for permitting or enhancing the encapsidation of a retroviral vector. The
CC vectors can be used for gene therapy, production of recombinant
CC polypeptides or production of transgenic animals
XX
SQ Sequence 578 BP; 94 A; 139 C; 172 G; 0 T; 173 U; 0 Other;
XX
Query Match 29.1%; Score 155; DB 2; Length 578;
Best Local Similarity 67.4%; Pred. No. 7e-42;
Matches 118; Conservative 51; Mismatches 5; Indels 1; Gaps 1;
XX
QY 360 GGGGCGCCCTCTACACATTTGTCAGTGGCGCCAGATTGCGATTGTAATAAG 419
DB 1 GGGGCGCCCTCTACACATTTGTCAGTGGCGCCAGATTGCGATTGTAATAAG 60
XX
QY 420 -CTTTTCTCTATATCTCAGATTGTCAGTGGCGCCAGATTGTCGTTGGCT 478
DB 61 UUU 120
XX
QY 479 GGGCTACTGGGTGGGAGTGGGATCCGAGTGAATCCGTAGTATTCGTTCAACA 533
DB 121 GGCCUACUGGGGUGGGGUGGCGGACUGAUAUCCGUAUUAUUAACA 175
XX
RESULT 11
AAQ76041
ID AAQ76041 standard; DNA; 3878 BP.
XX
AC AAQ76041;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Retrovirus vector pP0115-R1.
XX
KM Retrovirus; vector; pP0115-R1; spleen necrosis virus; SNV; gene transfer;
KM gene therapy; ss.
XX
OS Spleen necrosis virus.
XX
PN WO9429437-A1.
XX
PD 22-DEC-1994.
XX
PF 07-JUN-1994; 94MO-US006415.
XX
PR 07-JUN-1993; 93US-00073345.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Dornburg RC;
XX
DR MPI, 1995-036467/05.
XX
PT Recombinant retrovirus vector, contg. non-retroviral gene, - has ability
PT to produce progeny virus, in helper cell which can infect host cell and
PT form provirus.
XX
PS Example; Page 17; 28pp; English.

XX
XX The universal retroviral vector pP0115-R1 (given in AAQ76041) was
CC obtained by replacing the SV40 promoter and hpt gene of pP011-R1
CC (AAQ76038) with the multiple cloning site of pBluescript II KS. The
CC vectors allow cell-type specific gene expression and eliminate risks of
CC downstream activation of cellular proto-oncogenes. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T; 0 U; 0 Other;
XX
Query Match 27.2%; Score 145; DB 2; Length 3878;
Best Local Similarity 90.4%; Pred. No. 4.9e-38;
Matches 189; Conservative 0; Mismatches 15; Indels 5; Gaps 3;
XX
QY 330 GCGTATATAGCCAGGCGATCTCTCGGGGTCGCGCTACACA---TTGTTG 386
DB 654 GTCATATATAGCCAGGCGATCTCTCGGGGTCGCGCTACACA---TTGTTG 713
XX
QY 387 ACGTGGCGCCAGATTGCAATCTGTATATAA-GCTTTTCTTATATCTCAGATTGG 445
DB 714 ACGTGGCGCCAGATTGCAATCTGTATATAA-GCTTTTCTTATATCTCAGATTGG 773
XX
QY 446 CAGTGAAGAGATTGTTGTCGTTGCTGCTGCGCTACTGCGTGG-GTAGGATCCG 504
DB 774 CAGTGAAGAGATTGTTGTCGTTGCTGCTGCGCTACTGCGTGG-GTAGGATCCG 833
XX
QY 505 GACTGAATCCGTAGTATTCGTTCAACA 533
DB 834 GACTGAATCCGTAGTATTCGTTCAACA 862
XX
RESULT 12
AAQ76038
ID AAQ76038 standard; DNA; 5528 BP.
XX
AC AAQ76038;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Retrovirus vector pP0111-R1.
XX
KM Retrovirus; vector; pP0111-R1; spleen necrosis virus; SNV;
KM cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
KM long terminal repeat; LTR; encapsidation; gene transfer; gene therapy;
KM ss.
XX
OS Spleen necrosis virus.
XX
PN WO9429437-A1.
XX
PD 22-DEC-1994.
XX
PF 07-JUN-1994; 94MO-US006415.
XX
PR 07-JUN-1993; 93US-00073345.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Dornburg RC;
XX
DR MPI, 1995-036467/05.
XX
PT Recombinant retrovirus vector, contg. non-retroviral gene, - has ability
PT to produce progeny virus, in helper cell which can infect host cell and
PT form provirus.
XX
PS Example; Page 13-14; 28pp; English.
XX
XX New recombination-free, highly efficient retroviral vectors pP011-R1
CC (given in AAQ76038), pP011-R2 (AAQ76039) and pP011-R3 (AAQ76040) were
CC obtained by replacing the U3 region of the left LTR of spleen necrosis
CC virus with the IE promoter/enhancer of CMV, and extension of the

Query Match	23.9%;	Score 127.6;	DB 2;	Length 5519;
Best Local Similarity	92.3%;	Pred NO	50-33.	

Matches 168; Conservative 0; Mismatches 9; Indels 5; Gaps 3;

QY 357 CTGGGGGTGGCCGCTCCACACA---TTGTGTGACGGGCGCCGACATTCGATCTGTA 413
 Db 672 CTGGGGGTGGCCGCTCCACACA---TTGTGTGACGGGCGCCGACATTCGATCTGTA 731
 QY 414 TAAAA-GCTTTTCTTATATCTCAGATTGCGAGTGAAGAGATTTTGTGCTG 472
 Db 732 TAAACCTTTTCTTATATCTCAGATTGCGAGTGAAGAGATTTTGTGCTG 791
 QY 473 TTGGCTGGCTTACTGAGTGGG-GTAGGATCCGAGCTGAATCCGTAGTATTCGTA 531
 Db 792 TTGGCTGGCTTACTGAGTGGG-GTAGGATCCGAGCTGAATCCGTAGTATTCGTA 851
 QY 532 CA 533
 Db 852 CA 853

RESULT 15

AAK91988/C
 ID AAK91988 standard; cDNA; 714 BP.

XX AAK91988;
 AC

XX 06-NOV-2001 (first entry)
 DT

XX Human cDNA 5'-end sequence, SEQ ID NO: 448.
 DE

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
 KM

XX Homo sapiens.
 OS

XX EPI130094-A2.
 PN

XX 05-SEP-2001.
 PD

XX 07-JUL-2000; 2000BP-00114089.
 PF

XX 08-JUL-1999; 99JP-00194486.
 PR

XX 11-JAN-2000; 2000JP-00118774.
 PR

XX 02-MAY-2000; 2000JP-00183765.
 PR

XX (HELI-) HELIX RES INST.
 PA

XX Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.

XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.

XX Claim 2; SEQ ID NO 448; 1380bp + Sequence Listing; English.
 PS

XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesized by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is the nucleotide sequence of the 5'-end of
 CC a cDNA provided in the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in CD-
 CC ROM format directly from EPO
 XX

XX Sequence 714 BP; 136 A; 215 C; 193 G; 167 T; 0 U; 3 Other;
 SQ

Query Match 6.3%; Score 33.8; DB 4; Length 714;
 Best Local Similarity 54.4%; Pred. No. 1.6;

Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 394 GCCCAGATTCGAATCTGTATATAAAGCTTTTCTTATATCTCAGATTGCGAGTGAGA 453
 Db 530 GTCAAAATTCCTCAGTACAAAAGCTAAATCTCAGATCAGCAGCTGCTTGAAT 471
 QY 454 GAGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 513
 Db 470 TAGATGTGTCTCTTGTCTTTTACCTCTCAGGGGACAGAGCTAAGGACGGGACAGGGC 411
 QY 514 CGTAG 518
 Db 410 CGAG 406

Search completed: May 25, 2004, 02:15:46
 Job time : 355 secs

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CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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LOCATION: (234187)..(234187)
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NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
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NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
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NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
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NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
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NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130988)..(1130988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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Query Match 6.0%; Score 32; DB 4; Length 9347;

```

1 ADDRESSER: ZymoGenetics, Inc.
2 STREET: 4225 Roosevelt Way, N.E.
3 CITY: Seattle
4 STATE: WA
5 COUNTRY: USA
6 ZIP: 98105
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patentin Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/206,176
15 FILING DATE:
16 CLASSIFICATION: 435
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Parker, Gary E
19 REGISTRATION NUMBER: 31-648
20 REFERENCE/DOCKET NUMBER: 93-15
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 206-548-8080 ext 322
23 TELEFAX: 206-548-2329
24 INFORMATION FOR SEQ ID NO: 3:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 8878 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: double
29 TOPOLOGY: linear
30 MOLECULE TYPE: DNA (genomic)
31 IMMEDIATE SOURCE:
32 CLONE: human fibrinogen B-beta chain
33 FEATURE:
34 NAME/KEY: misc RNA
35 LOCATION: 1..469
36 FEATURE:
37 NAME/KEY: exon
38 LOCATION: 470..583
39 FEATURE:
40 NAME/KEY: intron
41 LOCATION: 584..3257
42

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FEATURE:
NAME/KEY: exon
LOCATION: 3258..3449
FEATURE:
NAME/KEY: intron
LOCATION: 3450..3938
FEATURE:
NAME/KEY: exon
LOCATION: 3939..4122
FEATURE:
NAME/KEY: intron
LOCATION: 4123..5042
FEATURE:
NAME/KEY: exon
LOCATION: 5043..5270
FEATURE:
NAME/KEY: intron
LOCATION: 5271..5830
FEATURE:
NAME/KEY: exon
LOCATION: 5831..5944
FEATURE:
NAME/KEY: intron
LOCATION: 5945..6632
FEATURE:
NAME/KEY: exon
LOCATION: 6633..6758
FEATURE:
NAME/KEY: intron
LOCATION: 6759..6966
FEATURE:
NAME/KEY: exon
LOCATION: 6967..7252
FEATURE:
NAME/KEY: intron
LOCATION: 7253..7870
FEATURE:
NAME/KEY: exon
LOCATION: 7871..8102
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 8103..8537
FEATURE:
NAME/KEY: misc RNA
LOCATION: 8538..8878
FEATURE:
NAME/KEY: CDS
LOCATION: join(470..583, 3258..3449, 3939..4122, 5043..5270,
5831..5944, 6633..6758, 6967..7252, 7871..8102)
US-08-206-176-3

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Query Match          5.9%; Score 31.4; DB 1; Length 8878;
Best Local Similarity 57.7%; Pred. No. 3.5;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 84 AATATGCTGCTGCTGCTTACCGCCATGTAATGATATATTCGCTGATATCATTTCT 143
DB 1109 AAAAAGCAATATTTCAATTTTATATATACATGATGATATTTCTTTAGGCTTAACT 1050
QY 144 CGGAATCGGATCAAGGAGGAGGCTCAATAAACCTAA 180
DB 1049 TATATTTTATATATATGATATCTCAGTAACAATATA 1013

```

RESULT 5
US-08-943-731-1

```

; Sequence 1, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKO, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, IARISA

```

```

APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORRKO, JARMO
APPLICANT: ALA-KORRKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
STREET: PANITCH SCHWARZ JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18609 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-1

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Query Match          5.9%; Score 31.4; DB 3; Length 18609;
Best Local Similarity 53.7%; Pred. No. 5.7;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 398 AGATTCGATCTGTGATATAAGCTTTTCTTATATCTCTGATTTGGAGTGAAGAG 457
DB 5386 AGGTAAAGGCTGTCTGGAACATCATGCTCCACATCCCAAGATCCACATGAATGA 5345
QY 458 ATTTGTTGCTGGGCTGCTGCTACCTGAGGGGTGAGGATCCGAGCTGAATCCGTA 517
DB 5346 ATTTCTCATCATATATTTCTGATCTGATCAAGGGTGAGCTCGGAGCCCTGGTGAAAATGGA 5405
QY 518 G 518
DB 5406 G 5406

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RESULT 6

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US-09-453-702B-111/C
; Sequence 111, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie

```

```
/ Perna, Nicole T.
/ Plunkett, Guy
/ Welch, Rod
/ TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Quarles & Brady
/ STREET: 1 South Pinckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 8.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/453,702B
/ FILING DATE: 03-Dec-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/110,955
/ FILING DATE: 04-DEC-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960236.95017
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 251-5000
/ TELEFAX: (608) 251-9166
/ INFORMATION FOR SEQ ID NO: 111:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21119
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-453-702B-111

Query Match          5.8%; Score 30.8; DB 4; Length 21119;
Best Local Similarity 52.3%; Pred. No. 10;
Matches 68; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 176 ATAAAGGAATGTTTGTGAAGCAATCAGACCACTTGCACCTCAATACGAC 235
    |||||
DB 12614 ATTAATGTATTAATTAATACATAGAAAGCAAGCCAAAGTTAAACGTAATAATTATTAAC 12555
    |||||

QY 236 AATCAAGATCGAATCATATCTAGCCAAATGTTGTAAGGCGAGATCTATCTCC 295
    |||||
DB 12554 AAGTTTGTGTGTAATAAGATTGGGCGCAAAATTTGAAAAGGCTTGACATTCCTCCAT 12495
    |||||

QY 296 AATGAGGAA 305
    |||||
DB 12494 CATGCTGGA 12485
    |||||

RESULT 7
US-09-621-976-2813
/ Sequence 2813, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jober, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 2813
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/ LENGTH: 832
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 235..399
US-09-621-976-2813

Query Match          5.7%; Score 30.4; DB 4; Length 832;
Best Local Similarity 10.6%; Pred. No. 18;
Matches 28; Conservative 120; Mismatches 116; Indels 0; Gaps 0;

QY 64 ACTGCATATTAAGCTTCTGTAATCATGCTTGCCTTAGCCGCAATGTAATAT 123
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DB 110 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 169
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QY 124 ATTTGCTGATATCATTTCTCGAATGCGATCAAGCAGGCTCATAAACATAAAG 183
    |||||
DB 170 MACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 229
    |||||

QY 184 AATGTTTGTGAAGCAATCAGACCACTTGCACATCATCAATCAGAAACAGCA 243
    |||||
DB 230 RAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 289
    |||||

QY 244 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
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DB 290 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 349
    |||||

QY 304 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
    |||||
DB 350 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 373
    |||||

RESULT 8
US-10-204-708-45/C
/ Sequence 45, Application US/10204708
/ Patent No. 6677731
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIERENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
/ FILE REFERENCE: 5013.1012
/ CURRENT APPLICATION NUMBER: US/10/204,708
/ CURRENT FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: PCT/EP01/03971
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 45
/ LENGTH: 19233
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
/ NAME/KEY: unsure
/ LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228)
/ OTHER INFORMATION: n is a or g or c or t
/ NAME/KEY: unsure
/ LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
/ OTHER INFORMATION: n is a or g or c or t
/ FEATURE:
/ NAME/KEY: unsure
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NAME/KEY: unsure
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OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4298, 4363, 4610, 4627, 4675, 4693, 4698, 4738, 4777, 4781)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4787, 4825, 4829, 4838, 4855, 5462, 5494, 5496, 5500, 5674)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (5690, 5697, 5705, 5715, 5890, 5910, 5913, 6027, 6080, 6109)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (8059, 8075, 8632, 8636, 9700, 9717, 9815, 9818, 9867, 9879)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (10005, 10075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (11703, 11933, 12050, 12340, 12981, 13564, 13764..13765, 13787)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (13846, 14168, 16566, 17006, 17217, 17650, 17653, 17656, 17898)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (19200)
OTHER INFORMATION: n is a or g or c or t
US-10-204-708-45
Query Match 5.7%; Score 30.4; DB 4; Length 19233;
Best Local Similarity 56.7%; Pred. No. 13;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 169 ATAAACCATTAAGAAATGTTGTTGAGCAAGCATGACCACTTGACATCCAAAT 228
Db 17016 ATAAATAATTAACCAATATTAACCTACGCCATATATCTTAACATTTAAAAACCAA 16957
QY 229 CAGCAAAACAGCAAGTCAACTATATATCTGAGCC 265
Db 16956 ATAAAAAATCAGCAATCAAAAAATTAACCATCC 16920
RESULT 9
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
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NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (15001)-(30000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (75001)-(90000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (225001)-(240000)
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (705701) ..(720000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (735001) ..(750000)
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (795001) ..(810000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (810001) ..(825000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (855001) ..(870000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (870001) ..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (885001) ..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (900001) ..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

Query Match          5.7%; Score 30.4; DB 4; Length 1230025;
Best local similarity 54.5%; Pred. No. 1.5e+02;
Matches    61; Conservative   0; Mismatches    51; Indels      0; Gaps      0;

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DB      638954 GGAAATATATTCATGACATTTAAGAGGAAATTTGGCCTCACCCATAGGATACATATTAG 639012
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QY      77 CTCTGTATATCATGCTGCTTACCCTTAACCCGCAATGACTGTATATTTC 128
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DB      639014 CTTCACTCTCTTTTCCCTATGATGAGACTATTGAGAGCAATTTTC 639065
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RESULT 10
US-09-221-298-77/c
Sequence 77, Application US/09221298
Patent No. 6284241
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 77
LENGTH: 458
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Db 5805 GTCACGTGATGATGTCACAGCTGATTTGTGGCGCTTAACATAGTTGAG-CG 5747
Qy 390 TGGGCCCCCATTCGATCTGTATTAAGCTTTTCTTCTATATCTCG 440
Db 5746 CGAGAGCTTATGTTAGTATGATCTCTTTTTCACAGATTTACAG 5696

RESULT 13

US-08-816-346-5
; Sequence 5, Application US/08816346
; Patent No. 6127525
; GENERAL INFORMATION:
; APPLICANT: Crystal, Ronald G.
; APPLICANT: Falck-Pedersen, Erik
; APPLICANT: Gail, Jason
; APPLICANT: Kovesdi, Imre
; APPLICANT: Wickham, Thomas J.
; TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
; TITLE OF INVENTION: METHODS OF USING SAME
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA - 4900
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,346
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 67167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/616-5600
; TELEFAX: 312/616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-816-346-5

Query Match 5.6%; Score 30; DB 3; Length 603;
Best Local Similarity 55.9%; Pred. No. 2;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 97 TGCCTTAGCCGCATTTGATGATATTTGCTGATATCATTTCTCGAATCGCATC 156
Db 410 TGCTCTTCCAAAGTTGACTTGCAATCTTCTCAATACACTCTTTGAACGACCGGC 469
Qy 157 AAGAGCAGCTCATTAACCATTAAGAAATGTTTGTGAAG 198
Db 470 AAGGCATGCTACTTAACCAAAAGTGTTTGTACAGTGAAG 511

RESULT 14

US-09-335-411-5
; Sequence 5, Application US/09335411
; Patent No. 6153435
; GENERAL INFORMATION:
; APPLICANT: Crystal, Ronald G.
; APPLICANT: Falck-Pedersen, Erik
; APPLICANT: Gail, Jason

APPLICANT: Kovesdi, Imre
APPLICANT: Wickham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA - 4900
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,411
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,346
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600
TELEFAX: 312/616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-335-411-5

Query Match 5.6%; Score 30; DB 3; Length 603;
Best Local Similarity 55.9%; Pred. No. 2;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 97 TGCCTTAGCCGCATTTGATGATATTTGCTGATATCATTTCTCGAATCGCATC 156
Db 410 TGCTCTTCCAAAGTTGACTTGCAATCTTCTCAATACACTCTTTGAACGACCGGC 469
Qy 157 AAGAGCAGCTCATTAACCATTAAGAAATGTTTGTGAAG 198
Db 470 AAGGCATGCTACTTAACCAAAAGTGTTTGTACAGTGAAG 511

RESULT 15

US-08-816-346-1
; Sequence 1, Application US/08816346
; Patent No. 6127525
; GENERAL INFORMATION:
; APPLICANT: Crystal, Ronald G.
; APPLICANT: Falck-Pedersen, Erik
; APPLICANT: Gail, Jason
; APPLICANT: Kovesdi, Imre
; APPLICANT: Wickham, Thomas J.
; TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
; TITLE OF INVENTION: METHODS OF USING SAME
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA - 4900
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Searched: 2953838 seqs, 2272363821 residues

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Minimum DB seq length: 0

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	6.6	328	13	US-10-142-426-34
2	35	6.6	328	15	US-10-123-155-34
3	35	6.6	328	15	US-10-146-731-34
4	35	6.6	328	15	US-10-140-472-34
5	35	6.6	328	15	US-10-141-761-34
6	35	6.6	328	15	US-10-142-885-34
7	35	6.6	328	15	US-10-158-790-34
8	35	6.6	328	16	US-10-137-871-34
9	35	6.6	328	16	US-10-140-923-34
10	35	6.6	328	16	US-10-141-756-34
11	35	6.6	328	16	US-10-141-759-34
12	35	6.6	328	16	US-10-140-805-34
13	35	6.6	328	16	US-10-140-864-34
14	35	6.6	616	13	US-10-142-426-206

15	34	6.4	616	15	US-10-123-155-206	Sequence 206, App
16	34	6.4	616	15	US-10-146-731-206	Sequence 206, App
17	34	6.4	616	15	US-10-140-472-206	Sequence 206, App
18	34	6.4	616	15	US-10-141-761-206	Sequence 206, App
19	34	6.4	616	15	US-10-142-885-206	Sequence 206, App
20	34	6.4	616	15	US-10-158-790-206	Sequence 206, App
21	34	6.4	616	16	US-10-137-871-206	Sequence 206, App
22	34	6.4	616	16	US-10-140-923-206	Sequence 206, App
23	34	6.4	616	16	US-10-141-756-206	Sequence 206, App
24	34	6.4	616	16	US-10-141-759-206	Sequence 206, App
25	34	6.4	616	16	US-10-140-805-206	Sequence 206, App
26	34	6.4	616	16	US-10-140-864-206	Sequence 206, App
27	33.4	6.3	6617	13	US-10-449-462-1	Sequence 1, Appl1
28	33.4	6.3	6617	15	US-10-210-296-1	Sequence 112, Appl
29	32.8	6.2	802	15	US-10-184-644-312	Sequence 312, App
30	32.8	6.2	802	15	US-10-184-634-312	Sequence 312, App
31	32.8	6.2	25519	13	US-10-087-192-1207	Sequence 1207, Ap
32	32.6	6.1	650	13	US-10-027-632-1039	Sequence 1039, Ap
33	32.6	6.1	650	13	US-10-027-632-1040	Sequence 1040, Ap
34	32.6	6.1	650	13	US-10-027-632-1041	Sequence 1041, Ap
35	32.6	6.1	650	16	US-10-027-632-1040	Sequence 1039, Ap
36	32.6	6.1	650	16	US-10-027-632-1041	Sequence 1040, Ap
37	32.6	6.1	650	16	US-10-027-632-1041	Sequence 1041, Ap
38	32.6	6.1	96595	12	US-10-052-482-232	Sequence 232, App
39	32.2	6.0	3388	13	US-10-416-592-8	Sequence 8, Appl1
40	32.2	6.0	3410	15	US-10-120-988-225	Sequence 225, App
41	32.2	6.0	20346	5	US-10-123-9658-1	Sequence 1, Appl1
42	32	6.0	19319	13	US-10-424-599-27873	Sequence 27873, A
43	32	6.0	9347	13	US-10-204-708-36	Sequence 36, Appl
44	32	6.0	397658	9	US-09-813-320-3	Sequence 3, Appl1
45	31.4	5.9	601	13	US-10-027-632-89624	Sequence 89624, A

ALIGNMENTS

RESULT 1
US-10-142-426-34/c
; Sequence 34, Application US/10142426
; Publication NO. US20040048333A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Inc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C24
; CURRENT APPLICATION NUMBER: US/10/142,426
; PRIOR APPLICATION: removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-142-426-34
Query Match 6.6%; Score 35; DB 13; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;

Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

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Bb 322 BYR..M.TYNN..GHC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAGAAATGTTTGTGAAGCAAGCATCAGACCATTTGCAC 220
Bb 262 KYA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTHNRA.YA.AH 203
QY 221 CATCCATACGAAACAACGAGATCGAATCTACTACTGAGCCAAATGGTTGTAAGG 280
Bb 202 YN.KTN...NSSHSB...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCCATGAGGAGAAATGTCAATGCAACATCTGTAAAGCGCTATATAG 340
Bb 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKA CSBMYCCAN.Y..A 83
QY 341 CCAAGTGCATCTCTGCTCGGGGCGCGCTCCTACACATTTGTTGACGTGCGGCCAGA 400
Bb 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CM.S.B.B.SC.BB.MRTWMC.D.M.SN. 23
QY 401 TTC 403
Bb 22 .TS 20

RESULT 2
US-10-123-155-34/c
; Sequence 34, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; Prior Filing Date: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-34

Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

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Bb 322 BYR..M.TYNN..GHC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAGAAATGTTTGTGAAGCAAGCATCAGACCATTTGCAC 220
Bb 262 KYA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTHNRA.YA.AH 203

QY 221 CATCCATACGAAACAACGAGATCGAATCTACTACTGAGCCAAATGGTTGTAAGG 280
Bb 202 YN.KTN...NSSHSB...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCCATGAGGAGAAATGTCAATGCAACATCTGTAAAGCGCTATATAG 340
Bb 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKA CSBMYCCAN.Y..A 83
QY 341 CCAAGTGCATCTCTGCTCGGGGCGCGCTCCTACACATTTGTTGACGTGCGGCCAGA 400
Bb 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CM.S.B.B.SC.BB.MRTWMC.D.M.SN. 23
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Bb 22 .TS 20

RESULT 3
US-10-146-731-34/c
; Sequence 34, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C33
; CURRENT APPLICATION NUMBER: US/10/146,731
; Prior Filing Date: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-146-731-34

Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCGCGCATTTGATATATATTCGCTGATATATTCCTCGGAATCGGCATCAAGA 160
Bb 322 BYR..M.TYNN..GHC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAGAAATGTTTGTGAAGCAAGCATCAGACCATTTGCAC 220
Bb 262 KYA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTHNRA.YA.AH 203
QY 221 CATCCATACGAAACAACGAGATCGAATCTACTACTGAGCCAAATGGTTGTAAGG 280
Bb 202 YN.KTN...NSSHSB...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCCATGAGGAGAAATGTCAATGCAACATCTGTAAAGCGCTATATAG 340
Bb 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKA CSBMYCCAN.Y..A 83

QY 341 CCAAGTCATCTCTGCTCGGCGTCCGCTTACACATTTGTTGACGTGCGGCCGACA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 4
US-10-140-472-34/c

; Sequence 34, Application US/10140472
; Publication No. US20030138888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: US/10/140,472
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-472-34

Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCGCCATCTGATCTGATATATTTGCGTGAATATCATTTCTCGAATCGCATCAAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTGTTGAAGGCAAGCATCAGACCACTTGAC 220
Db 262 KVA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMBR.YA.AH 203
QY 221 CATCATATCAGCAACAAACAGATGAACTATCATCTAGGCAATGTTGTAAGGG 280
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRP...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCTGCTCGGCGTCCGCTTACACATTTGTTGACGTGCGGCCGACA 340
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKAESBMYCCAN.Y..A 83
QY 341 CCAAGTCATCTCTGCTCGGCGTCCGCTTACACATTTGTTGACGTGCGGCCGACA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 5
US-10-141-761-34/c
; Sequence 34, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C198
; CURRENT APPLICATION NUMBER: US/10/141,761
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-761-34

Query Match 6.6%; Score 35; DB 15; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCGCCATCTGATCTGATATATTTGCGTGAATATCATTTCTCGAATCGCATCAAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTGTTGAAGGCAAGCATCAGACCACTTGAC 220
Db 262 KVA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMBR.YA.AH 203
QY 221 CATCATATCAGCAACAAACAGATGAACTATCATCTAGGCAATGTTGTAAGGG 280
Db 142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKAESBMYCCAN.Y..A 83
QY 341 CCAAGTCATCTCTGCTCGGCGTCCGCTTACACATTTGTTGACGTGCGGCCGACA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWMC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 6
US-10-142-885-34/c
; Sequence 34, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; PRIORITY FILING DATE: 2002-05-10
; PRIOR Application removed - See File Wrapper or Palm
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-885-34

Query Match
Best Local Similarity 6.6%; Score 35; DB 15; Length 328;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

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QY 101 TTAGCCGCGCATTTGATGATATATTTGCGTGAATATCTTTCGGAATCGGCATCAGA 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S..N.S..Y.SDK. 263
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 161 GCAGGCTCATTAACATTAAGAAATGTTGTAAGGCAAGCATGACCACTTGCAC 220
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 KYA..RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTHNRA.YA..AH 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 221 CATCAATCAGAACAAACAGAGATCATATCATATGAGCAATGTTGTAAGGG 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YN.KYN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 CAGATGCTATCTCCATGAGGAAATGTCATCAACATCTGTGAAGCGGCTATATAAG 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 C.SH.SC.D.Y...YDSRAK.CCS..NB.D.MH.Y.SBDYCANRKAOSBMYYCCAN.Y..A 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 CCAGGTCATCTTGTGCTCGGCGTCCGCTCATACATATGTTGTGACGTGCGGCCAGA 400
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWVC.D.M.SN. 23
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 401 TTC 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 .TS 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 7
US-10-158-790-34/c
; Sequence 34, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; PRIORITY FILING DATE: 2002-05-10
; PRIOR Application removed - See File Wrapper or Palm
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-790-34

Query Match
Best Local Similarity 6.6%; Score 35; DB 15; Length 328;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

```

```

QY 101 TTAGCCGCGCATTTGATGATATATTTGCGTGAATATCTTTCGGAATCGGCATCAGA 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN...B.Y.NHSKS...S..N.S..Y.SDK. 263
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 161 GCAGGCTCATTAACATTAAGAAATGTTGTAAGGCAAGCATGACCACTTGCAC 220
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 KYA..RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTHNRA.YA..AH 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 221 CATCAATCAGAACAAACAGAGATCATATCATATGAGCAATGTTGTAAGGG 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YN.KYN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 CAGATGCTATCTCCATGAGGAAATGTCATCAACATCTGTGAAGCGGCTATATAAG 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 C.SH.SC.D.Y...YDSRAK.CCS..NB.D.MH.Y.SBDYCANRKAOSBMYYCCAN.Y..A 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 CCAGGTCATCTTGTGCTCGGCGTCCGCTCATACATATGTTGTGACGTGCGGCCAGA 400
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWVC.D.M.SN. 23
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 401 TTC 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 .TS 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 8
US-10-137-871-34/c
; Sequence 34, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C153
; CURRENT APPLICATION NUMBER: US/10/137,871

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Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-871-34

Query Match
Best Local Similarity 6.6%; Score 35; DB 16; Length 328;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

101 TTAGCCGCATTTACTGATATATTTCCGTATATCTTCGATCGCATCAGA 160
BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263
161 GCAGGCTCATTAACCAAGAAAGAAATGTTGTAAGGCAAGCATCAGACCTGCAC 220
KVA..RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMPRA.VA.AH 203
221 CATCCATCAGCAACCAAGCAAGATCACTATCATCTAGCCATGCTTGAAGGG 280
YN.KYN...NSHSEB...SBBB.CN.SMTT.ABNAR..DNRD...B.CG.T.CN..D.S 143
202 YN.KYN...NSHSEB...SBBB.CN.SMTT.ABNAR..DNRD...B.CG.T.CN..D.S 143
281 CAGATGCTATCTTCATGAGGAGAAATGTCATCACTCTGTGAAGCGCTATATAG 340
142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKCABMYCCAN.Y..A 83
341 CAGATGCTATCTTCGTCGCGGTCGCGCTCTACATCTGTTGTGACGTCGCCAGCA 400
H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SB.MRTWMC.D.M.SN. 23
82 ..H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SB.MRTWMC.D.M.SN. 23
401 TTC 403
22 .TS 20

RESULT 9

US-10-140-923-34/c
Sequence 34, Application US/10140923
Publication No. US20030207355A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C188
CURRENT APPLICATION NUMBER: US/10/140,923
PRIORITY FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-923-34

Query Match 6.6%; Score 35; DB 16; Length 328;

Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

101 TTAGCCGCATTTACTGATATATTTCCGTATATCTTCGATCGCATCAGA 160
BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263
161 GCAGGCTCATTAACCAAGAAAGAAATGTTGTAAGGCAAGCATCAGACCTGCAC 220
KVA..RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMPRA.VA.AH 203
221 CATCCATCAGCAACCAAGCAAGATCACTATCATCTAGCCATGCTTGAAGGG 280
YN.KYN...NSHSEB...SBBB.CN.SMTT.ABNAR..DNRD...B.CG.T.CN..D.S 143
202 YN.KYN...NSHSEB...SBBB.CN.SMTT.ABNAR..DNRD...B.CG.T.CN..D.S 143
281 CAGATGCTATCTTCATGAGGAGAAATGTCATCACTCTGTGAAGCGCTATATAG 340
142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKCABMYCCAN.Y..A 83
341 CAGATGCTATCTTCGTCGCGGTCGCGCTCTACATCTGTTGTGACGTCGCCAGCA 400
H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SB.MRTWMC.D.M.SN. 23
82 ..H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SB.MRTWMC.D.M.SN. 23
401 TTC 403
22 .TS 20

RESULT 10

US-10-141-756-34/c
Sequence 34, Application US/10141756
Publication No. US20030207359A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
PRIORITY FILING DATE: 2002-05-08
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-756-34

Query Match 6.6%; Score 35; DB 16; Length 328;
Best Local Similarity 6.9%; Pred. No. 0.67;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

101 TTAGCCGCATTTACTGATATATTTCCGTATATCTTCGATCGCATCAGA 160
BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S.N.S..Y.SDK. 263
161 GCAGGCTCATTAACCAAGAAAGAAATGTTGTAAGGCAAGCATCAGACCTGCAC 220
KVA..RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTNMPRA.VA.AH 203
221 CATCCATCAGCAACCAAGCAAGATCACTATCATCTAGCCATGCTTGAAGGG 280
YN.KYN...NSHSEB...SBBB.CN.SMTT.ABNAR..DNRD...B.CG.T.CN..D.S 143
202 YN.KYN...NSHSEB...SBBB.CN.SMTT.ABNAR..DNRD...B.CG.T.CN..D.S 143
281 CAGATGCTATCTTCATGAGGAGAAATGTCATCACTCTGTGAAGCGCTATATAG 340
142 C.SH.SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKCABMYCCAN.Y..A 83
341 CAGATGCTATCTTCGTCGCGGTCGCGCTCTACATCTGTTGTGACGTCGCCAGCA 400
H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SB.MRTWMC.D.M.SN. 23
82 ..H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SB.MRTWMC.D.M.SN. 23
401 TTC 403
22 .TS 20

Db 262 KYA.RB.MNK..MSTA.RG...AKSCHRA..SSA..R....N.C...RTHNMA.YA.AH 203
QY 221 CATCCAAATCAGCAACAACAGAGATGCAATCTATCTACAGCAGCCATGTTGTAAGG 280
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCTCAATGAGGAAATGTCATGCAACATCTGTAAAGCGGCTATATAAG 340
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y.A 83
QY 341 CCAAGTGCATCTCTGCTCGGGGTCGCCCTACACATCTGTGACGTGGGCCCA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 11

US-10-141-759-34/c
Sequence 34, Application US/10141759
Publication No. US20030207361A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C197
CURRENT APPLICATION NUMBER: US/10/141,759
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-759-34

Query Match Best Local Similarity 6.6%; Score 35; DB 16; Length 328;
Matches 21; Conservative 99; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCCGCATTTGATCTGATATATTTCCGCTGATATCATTTTCGGAAATCGGCATCAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTTGTGAAGCAAGCATCAGACCACTTGAC 220
Db 262 KYA.RB.MNK..MSTA.RG...AKSCHRA..SSA..R....N.C...RTHNMA.YA.AH 203
QY 221 CATCCAAATCAGCAACAACAGAGATGCAATCTATCTACAGCAGCCATGTTGTAAGG 280
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCTCAATGAGGAAATGTCATGCAACATCTGTAAAGCGGCTATATAAG 340
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y.A 83

QY 341 CCAAGTGCATCTCTGCTCGGGGTCGCCCTACACATCTGTGACATTTGACGCGCCCA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 12

US-10-140-805-34/c
Sequence 34, Application US/10140805
Publication No. US20030207417A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C176
CURRENT APPLICATION NUMBER: US/10/140,805
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-805-34

Query Match Best Local Similarity 6.6%; Score 35; DB 16; Length 328;
Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

QY 101 TTAGCCCGCATTTGATCTGATATATTTCCGCTGATATCATTTTCGGAAATCGGCATCAGA 160
Db 322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS....S.N.S..Y.SDK. 263
QY 161 GCAGGCTCATTAACCAATAAAGAAATGTTTGTGAAGCAAGCATCAGACCACTTGAC 220
Db 262 KYA.RB.MNK..MSTA.RG...AKSCHRA..SSA..R....N.C...RTHNMA.YA.AH 203
QY 221 CATCCAAATCAGCAACAACAGAGATGCAATCTATCTACAGCAGCCATGTTGTAAGG 280
Db 202 YN.KYN...NSSHBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143
QY 281 CAGATGCTATCTCTCAATGAGGAAATGTCATGCAACATCTGTAAAGCGGCTATATAAG 340
Db 142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRACSBMYCCAN.Y.A 83
QY 341 CCAAGTGCATCTCTGCTCGGGGTCGCCCTACACATCTGTGACATTTGACGCGCCCA 400
Db 82 ...H..KDSA..NB.S.YMCBSG.NMTSNB.CW.S.B.B.SC.BB.MRTWC.D.M.SN. 23
QY 401 TTC 403
Db 22 .TS 20

RESULT 13

US-10-140-864-34/C

Sequence 34, Application US/10140864

Publication No. US20030207419A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P33081C184

CURRENT APPLICATION NUMBER: US/10/140,864

CURRENT FILING DATE: 2002-05-07

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 34

LENGTH: 328

TYPE: PRT

ORGANISM: Homo Sapien

US-10-140-864-34

Query Match

Best Local Similarity 6.9%; Pred. No. 0.67;

Matches 21; Conservative 98; Mismatches 184; Indels 0; Gaps 0;

101 TTAGCCGCGCATTTGATGATATTTTCGCTGATATTCATTTCTCGAATCGGCATCAGA 160

322 BYR..M.TYNN.GHMC..S.N.NAY.GYNN..B.Y.NHSKS...S..N.S..Y..SDK. 263

161 GCAGGCTCATTAACCAATTAAGGAATGTTGTTGAAGGCAAGCATCAGACCTTCGAC 220

262 KYA..RB..MNR..MSTA..RG..AKSCHRA..SSA..R...N.C...RTHMRA.VA.AH 203

221 CATCCATCATGCAACAAACGAGATGATCATATCATGAGCCATGTTGTTAAAGG 280

202 YN.KTN...NSSHSBM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S 143

281 CAGATGCTATCTTCATGAGGAAATGTCATCAATCTCTGTAAGCGCTATATATAG 340

142 C.SH..SC.D.Y...YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKAOSBNVCAN.Y..A 83

341 CCGAGTGCATCTCTGCTCGGGTCCGCTCTACATATGTTGTGACGTGGCCCAAGA 400

82 ...H..KDSA..NB.S.YMCBSG.NMYSNB.CW.S.B.B.SC.BB..MRTWMC.D.M.SN. 23

401 TTC 403

22 .TS 20

Db

RESULT 14

US-10-142-426-206

Sequence 206, Application US/10142426

Publication No. US20040048333A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers, Luc

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P33081C224

CURRENT APPLICATION NUMBER: US/10/142,426

CURRENT FILING DATE: 2002-05-09

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 206

LENGTH: 616

TYPE: PRT

ORGANISM: Homo Sapien

US-10-142-426-206

Query Match

Best Local Similarity 9.6%; Pred. No. 2.1;

Matches 46; Conservative 124; Mismatches 308; Indels 0; Gaps 0;

18 GGGGAATGCGGAGGAGGAGCGCGGGGGAATAGCGGCTCGCTCATATTCATATAGC 77

8 RESVNRFGTYPALPSKGGKKEWELNFOYERAKKAASIKLGLERFHVGLGFSAE 67

78 TTCTGTAATCATGCTCTTCTGCTTACCGCCATTTGATATTTTCGCTGATATTC 137

68 WFTTAVGAILAGGLCVGIYATNSABACQYITNAKNILLVENDQQLKLSIPQSLBP 127

138 ATTTTCGGAATCGGATCAAGAGCGCTCATTAACCAATTAAGGAATGTTGTTGAA 197

128 LKAIIQYRLPMKKNNNLYSWDDFMEIGRSIPDQLBQVIESORANCAVALYISGTTGIP 187

198 GGAAGATGAGACCACTTCGACCATCATCAACGAACAAACGAGATGAATCATAT 257

188 KGWLSHDNITWTAGATTKDFKLTDRHETVSYLPSHIAQMDIWPPIKIGALTYFAQ 247

258 ACTGAGCCATGCTTGTAAAGGCGAGATGCTATCTTCATGAGGAAATGTCATGCA 317

248 ADALKTIVSTLKEVPTVPIGVPIWEKIHENVKNSAKSMGLKKAFVMAINIGPKVN 307

318 CATCTGTAAAGCGCTATATTAAGCGAGTGCATCTCTGCTCGGGGCTCGCTCATAC 377

308 SKMLGKYNTPVRYMAKTLVFSKVTSLGLDCHSFISGTAFLNDETAFFPLSDIPIG 367

378 ATTGTTGACGCGCGCCCAAGTTGGAATCTGTATTAAGAGCTTTTCTCTATATCC 437

368 ELVGLSESSGPHITISNONNRLISCGKILTGCKNMLPQONKXIDIGEICLMGRHIFMYLYE 427

438 CAGATGCGAGTGAAGAGATTTTGTCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCT 495

428 SETETTEALIDDEGMLHSGDLGGLDGLFLYVTHIHEILLTAGENVPPIPVETLVAK 485

Db

RESULT 15

US-10-123-155-206

Sequence 206, Application US/10123155

Publication No. US20030068794A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers, Luc

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

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APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

APPLICANT: DeForge, Laura

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 01:20:42 ; Search time 2498 Seconds

(without alignments)
6371.714 Million cell updates/sec

Title: US-10-623-891-2

Perfect score: 533

Sequence: 1 tctgaggagagagctccggg.....cgtgagtttcggtacacac 533

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:
1: em_estbda:*
2: em_estbun:*
3: em_estlin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estun:*
16: em_estm:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.4	7.4	1201	9	AL549619
2	38.2	7.2	621	28	BH767965
3	37.8	7.1	654	12	B1870967
4	37.4	7.0	1265	10	BF128543

Result No.	Score	Query Match	Length	ID	Description
5	37	6.9	745	29	BX184525
6	36.6	6.9	1201	13	BX381961
7	36.4	6.8	636	28	AZ572287
8	36.4	6.8	999	29	CNS00H4
9	35.8	6.7	1201	9	AL525502
10	35.4	6.6	456	12	B1350586
11	35.2	6.6	339	12	B1308473
12	35.2	6.6	595	28	BH567971
13	35.2	6.6	798	28	B2069169
14	35.2	6.6	852	28	CG928645
15	35.2	6.6	962	29	CNS00L9Z
16	35.2	6.6	1101	29	CNS00D8
17	35	6.6	584	28	AQ318844
18	35	6.6	787	13	B2992571
19	35	6.6	1040	13	BX155200
20	34.6	6.5	456	28	AQ538821
21	34.6	6.5	458	28	AQ641009
22	34.6	6.5	707	28	B2035991
23	34.6	6.5	1101	29	CNS0160P
24	34.6	6.5	1201	9	AL514124
25	34.4	6.5	539	9	AA504855
26	34.4	6.4	384	28	AQ410136
27	34.2	6.4	500	28	AQ559853
28	34.2	6.4	543	14	CA871192
29	34.2	6.4	616	28	B2953077
30	34.2	6.4	740	28	AQ888634
31	34.2	6.4	838	28	CG674752
32	34	6.4	479	28	AZ164493
33	34	6.4	559	29	CE737197
34	34	6.4	850	29	CG248501
35	34	6.4	898	29	CG248509
36	33.8	6.3	370	9	AV654960
37	33.8	6.3	429	29	CE523584
38	33.8	6.3	494	12	BG275671
39	33.8	6.3	549	13	BQ701682
40	33.8	6.3	623	28	BH765785
41	33.8	6.3	693	28	AQ372284
42	33.8	6.3	892	29	CNS04GZL
43	33.8	6.3	1200	9	AL564823
44	33.8	6.3	1201	9	AL557303
45	33.8	6.3	1842	29	CG756078

ALIGNMENTS

RESULT 1
LOCUS AL549619
DEFINITION AL549619 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD1055Y113 5-PRIME, mRNA sequence.
ACCESSION AL549619
VERSION AL549619.2 GI:31271437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12885780.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8081.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOD1055ABO70P1c1cluster=8081.r. Contact: Peng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/InvitrogenCorporation1600
Paradise Avenue Genoscope Sequence ID : CS001055AE070P1.
Location/Qualifiers

FEATURES

source

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001055Y113"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 7.4%; Score 39.4; DB 9; Length 1201;
Best Local Similarity 41.3%; Pred. No. 0.83;
Matches 74; Conservative 24; Mismatches 81; Indels 0; Gaps 0;

QY 146 GAATCGCATCAAGAGCAGGCTCTAATACATTAAGAAATGTTGTGAGGCAAGCA 205
DB 1022 GAACTGGTCTAAAGAGCAGGCTCTAATACATTAAGAAATGTTGTGAGGCAAGCA 1081
QY 206 TCAGACCACTTGCACATCCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 265
DB 1082 AGAATCCATCTTGTCTCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1141
QY 266 AATGTTGTAAAGGAGGAGTCTTCTCAATCAAGCAAGCAAGCAAGCAAGCAAGCA 324
DB 1142 HGGGGGGAAGGAGGAGTCTTCTCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1200

RESULT 2
BH767965/c 621 bp DNA linear GSS 20-MAR-2002
LOCUS BH767965
DEFINITION BMBAC37240477 PSU Brugia malayi genomic Bac Library 3 Brugia malayi genomic, genomic survey sequence.

ACCESSION BH767965.1 GI:19565729
VERSION BH767965.1
KEYWORDS GSS.
SOURCE Brugia malayi
ORGANISM Brugia malayi

REFERENCE 1 (bases 1 to 621)
AUTHORS Whitton,C., Daud,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster,J., Guilliano,D., Slatko,B. and Blaxter,M.
COMMENT Genome survey sequences from the human parasitic nematode Brugia malayi

JOURNAL Unpublished (2000)
COMMENT Contact: Blaxter M.
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JF, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, IACPB, University of Edinburgh, Edinburgh, UK.
Seq primer: 17 (TAAATACAGCTCATATAGGGG)
Class: BAC ends.

FEATURES

source

1..621
Location/Qualifiers
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"

/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/note="Vector: pBAC3.6; Site 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed by Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

ORIGIN

Query Match 7.2%; Score 38.2; DB 28; Length 621;
Best Local Similarity 52.1%; Pred. No. 1.5;
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 117 TGTATATATTTGGCTGATATCATTTCTCGGATCGGATCAAGACAGGCTCATTAACA 176
DB 171 TGAATATATTTAGGGGATTAATTTGGTCAAAATCTAATTAATGTTAAGATTGTAAATGA 112
QY 177 TAAAGAAATGTTGTTGAGGCAAGCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 236
DB 111 AATATATATTTTCTTAAAGAAATTTTAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCA 52
QY 237 AACACGATTCGAATCATATCTGAGCCATGTTTAAAG 279
DB 51 ATCACTTGAATGATGTTTACCGCCGTAATGAATGATG 9

RESULT 3
BI870967 654 bp mRNA linear EST 11-OCT-2001
LOCUS BI870967
DEFINITION 603395724F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:5405813 5', mRNA sequence.

ACCESSION BI870967.1 GI:16044640
VERSION BI870967.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 654)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12034 row: P column: 06
High quality sequence stop: 510.

FEATURES

source

1..654
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5405813"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally, oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 7.1%; Score 37.8; DB 12; Length 654;

Best Local Similarity 51.5%; Pred. No. 2.1;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 85 ATGATGTTGCTGCTTACCGCCATTGATGATATATTTGGCTGATATCTTTCTC 144
DB 461 ATTACTCTCTGTATCTTTAACTGATTTGGGTTTAACTTAAATTTTATCTTTATTT 520
QY 145 GGAATCGGATCAAGACAGGCTCATTAACCATTAAGAAATTTGTTGAAGCAAGC 204
DB 521 TTTTGGCACTCAAG 580
QY 205 ATGAGACCACTTGACCATTCATTCAGCAACAAACAGAGATGCACTA 253
DB 581 AAGCAACATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 629

RESULT 4
BF128543/c 1265 bp mRNA linear EST 24-OCT-2000
LOCUS 60181069OR1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053479 3',
DEFINITION mRNA sequence.
ACCESSION BF128543
VERSION BF128543.1 GI:10967583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1265)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LINC892 row: d column: 24
High quality sequence start: 25
High quality sequence stop: 124.
Location/Qualifiers
1. 1265
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4053479"
/issue_type="telomysarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 7.0%; Score 37.4; DB 10; Length 1265;
Best Local Similarity 58.6%; Pred. No. 3.7;
Matches 65; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 343 AGGTGATCTCTGCTGGGGTCCCTCTTCAATGTTTGTGACGTGGCCCAAT 402
DB 836 AAGGGGTTTGAGCTTCTTGCGGGATGATATTAATTAAGTCCGCCCACTCTGTA 777
QY 403 CGAATGTATAAAGCTTTTCTTATATCTCAGATTGACATGAGA 453

DB 776 TAACTCGTATATGCTGTATCTCCCCACAGAGATGATAGAGAGA 726

RESULT 5
BX184525 745 bp DNA linear GSS 28-JAN-2003
LOCUS BX184525
DEFINITION Danio rerio genomic clone DKEX-186F13, genomic survey sequence.
ACCESSION BX184525
VERSION BX184525.1 GI:28016395
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 745)
AUTHORS Humphrey, S.J., Huckle, E. and Durham, J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 186F13. 186F13
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. 745
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-186F13"
/issue_type="Testis"
/note="vector pindigobAC-536"

ORIGIN
Query Match 6.9%; Score 37; DB 29; Length 745;
Best Local Similarity 53.0%; Pred. No. 4;
Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 49 AGCGTGGCTGCTAACTGCAATTAAGCTTGTATCAAGCTTGCTTACGCGC 108
DB 164 AGGCGTGTATCTTTGATATATAGAAATATCTTGTCGACAGATCCCCAGCAGG 223
QY 109 CATTTACTGATATATTTGGCGATATCTTTCTCGAATCGCATCAAGAGCTC 168
DB 224 GTTTATTTAGATTATTTAGTAATTTGTAATTTCTGTGCAATTCGTGCAATGGAAG 283
QY 169 ATTAACCATTAAGAAATGTTGTGAA 197
DB 284 TTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 312

RESULT 6
BX381961/c 1201 bp mRNA linear EST 08-MAY-2003
LOCUS BX381961 Homo sapiens PLACENTA_COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD1072YF05 3-PRIME, mRNA sequence.
ACCESSION BX381961
VERSION BX381961.1 GI:30453007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genome
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://falllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope Sequence ID : CS0D1072CC03NP1.

FEATURES

source

1. 1201
Location/Qualifiers

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1072YF05"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (drr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Query Match      6.9%; Score 36.6; DB 13; Length 1201;
Best Local Similarity 2.8%; Pred. No. 6.5;
Matches 13; Conservative 143; Mismatches 302; Indels 0; Gaps 0;

QY 12 GCTCCGGGGAATGTGGAGGAGGCTCCGGGGGGAATAGCGTGCCTGCTACTGCCAT 71
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 905 GGGGKKKKMMYKKKKMMKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 71
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 ATTAGCTTCTGTAATCATGCTTCTTGCCTTAGCCGCACTTGTATATATTTGGCT 131
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 845 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 131
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 GATATCATTTCTCGGAATCGGATCAAGAGCGGCTCTAAACCTAAAGAAATGTTT 191
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 191
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 GTTGAAGCAACATCAGACCACTTGCACCACTCAACAGACAAACAGAGATCGAAC 251
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 ANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 251
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 252 TATCATCTGAGCCCAATGTTGTAAGGAGAGATGCTATCTCAATGAGGAAATGTC 311
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 311
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 312 ATGCAACATCTGTAAAGCGGCTATATAAGCAGGTGATCTTCTCGGCGCCGCTC 371
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 371
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 372 CTACACATTTGTTGACGCTGGCCAGATTGATCTGTAATTAAGCTTTTCTCTTA 431
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 431
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 432 TATCTCAGATTGGCAGTGAAGAGATTGTTGTCGTG 469
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 469
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7
A2572287/c 636 bp DNA linear GSS 15-MAY-2001
LOCUS A2572287 304Pv003 Pv MBN #30 Plasmodium vivax genomic 3', genomic survey
DEFINITION
ACCESSION A2572287.1 GI:13985224
VERSION A2572287.1
KEYWORDS
SOURCE Plasmodium vivax (malaria parasite P. vivax)
ORGANISM
REFERENCE
1 (bases 1 to 636)
AUTHORS Carillon,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT
Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida

2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.ufl.edu
Seq primer: M13(-20) forward
Class: Shotgun.

FEATURES

source

1. 636
Location/Qualifiers

```
/organism="Plasmodium vivax"
/mol_type="genomic DNA"
/strain="Salvador I (Collins, W. 1972. J. Parasitol. 69, 497-598)"
/db_xref="taxon:5855"
/dev_stage="asexual blood forms"
/lab_host="Salimiri boliviensis"
/clone_lib="Pv MBN #30"
/note="Vector: pBluescript SK(+) vector DNA, phagemid  
excised from lambda ZAP, Site 1: EcoR V, Site 2: EcoR V;  
Host leukocytes were extracted from P. vivax infected  
blood using the following methods: first, infected blood  
was activated by the following methods: first, infected blood  
per 10 ml blood. Then blood was passed over a column of  
acid washed 0.1 mm glass beads, then through a Plasmidiput  
filter, followed by passage through a column of pre-wet  
Whatman CRI1 powder (1:2 ratio volume of blood to CRI1,  
and finally centrifuged through a 50% Percoll density  
cushion. Purified DNA was digested with mung bean nuclease  
in the presence of 44% formamide at 500C as described  
(Verlick, K.D., Imbersek, R.B., and McCutchan, T.F. 1988.  
Nucleic Acids Research 16:6883-6896). Digested DNA was  
blunt-ended using T4 DNA Polymerase and size fractionated  
over a Sepharose CL-2B column. Fractions in the size range  
500bp-4kb were ligated into the Eco RV site of pBluescript  
SK(+), and E. coli XL-10 Gold transformed with the  
ligation mixture."
```

ORIGIN

```
Query Match      6.8%; Score 36.4; DB 28; Length 636;
Best Local Similarity 50.6%; Pred. No. 5.8;
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 31 GGAAGCTCGGGGGAATAGCGCTGCTGCTAATGCTATGCTTGTATCATG 90
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 607 GGGTCCCTCCGGTGCTCTCCCGGGGCTCCCGGGGGTCTCCCTTGGTAACTTTT 90
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 91 CTTCGCTGCTTAGCGGCACTTGTATGATATATTTGCTGATATGATTTCTCGAATC 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 547 TTTTTCCTCCCTATGCTGCTTGGAATAAATTAACCGCTGCGTCACTCAGTGTAG 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 151 GGCATCAAGACGAGGCTCATTAACCATTAAGAAATGTTTGTGAAGGAC 204
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 487 GGAATGATGAGAGAGAAAAAACAACAGGGAATTCATGTGACAGGAAAC 204
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 8
CNS00HK4/c 999 bp DNA linear GSS 03-JUN-1999
LOCUS CNS00HK4 999Pv003 Pv MBN #30 Drosophila melanogaster genome survey sequence 77 end of BAC:
DEFINITION BACR35P15 of RP11-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL073686.1 GI:4953365
VERSION AL073686.1
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM
REFERENCE
1 (bases 1 to 999)
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

/clone="IMAGE:4955382"
 /sex="mixed male and female"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="E. coli DH10B"
 /clone_lib="zebrafish adult brain"
 /note="Vector: pZIRPOX; Site 1: NotI; Site 2: SalI;
 Original library was constructed in lambdaZIRPOX. Mass
 excision of the cDNA library was performed to yield
 pZIRPOX plasmids. Insert check was done in original
 library."

ORIGIN

Query Match

Best Local Similarity 6.6%; Score 35.4; DB 12; Length 456;
 Matches 78; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 49 AGCGCTGAGTGGCAATGATGCTTGTGATATCATGCTTGCCTTACCGCC 108
 Db 308 AGGCTGATCTTTATGATATATAGAAATGCTTGTCTGCAGATCTCCAGCAGG 367
 QY 109 CATTGACTGATATATTTGCTGATATCATTTCTCGAATCGGATCAAGAGCAGCTC 168
 Db 368 GTTTATTGATTTATTTAGTCAATATTAAGTTTGGAAATCTGTCATTGGAAGAAG 427
 QY 169 ATAAACATTAAGAAAGTTTGTGAA 197
 Db 428 TTCTTTCAGAAAGAACCGTTTGTGAA 456

RESULT 11

BI308473
 LOCUS

DEFINITION EST529883 GP0D Medicago truncatula cDNA clone GP0D-7A11 5' end,

ACCESSION BI308473

VERSION BI308473.1 GI:14982800

KEYWORDS EST

SOURCE Medicago truncatula (barrel medic)

ORGANISM

REFERENCE
 AUTHORS Grusak M.A., Samac, D.A., Town, C.D., Van Aken, S., Uterback, T.,
 TITLE Cho, J. and Fraser, C.M.
 JOURNAL ESTs from developing reproductive tissues of Medicago truncatula
 COMMENT Unpublished (2001)

1 (bases 1 to 339)
 Grusak M.A., Samac, D.A., Town, C.D., Van Aken, S., Uterback, T.,
 Cho, J. and Fraser, C.M.
 ESTs from developing reproductive tissues of Medicago truncatula
 Unpublished (2001)

Contact: Michael A. Grusak
 USDA/ARS Children's Nutrition Research Center
 Baylor College of Medicine
 1100 Bates Street, Houston, TX 77030-2600, USA
 Tel: 713-798-7044
 Fax: 713-798-7078
 Email: mgrusak@bcm.tmc.edu

BI308473

71GR sequence name: MTOA006TK

More information is available at: www.medicago.org
 Seq primer: SKmod (CTA GAA CTA gtc gat CC).

Location/Qualifiers

FEATURES

source

1..339
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /cui_xref="A17"
 /db_xref="taxon:3880"
 /clone="GP0D-7A11"
 /tissue_type="immature pod wall"
 /dev_stage="immature pods, ranging in age from 15 to 30
 days after pollination"
 /clone_lib="GP0D"
 /note="Vector: pBluescript SK-; Site 1: BcoRI; Site 2:
 XhoI; Immature pods, ranging in age from 15 to 30 days

after pollination, were collected from greenhouse-grown
 plants. At harvest, seeds were removed from pods and
 isolated pod walls were collected and immediately frozen
 in liquid nitrogen. Pod walls were pooled for mRNA
 extraction. cDNA was prepared from polyA+ enriched RNA.
 The cDNA was directionally ligated into the Unizap XR
 vector from Stratagene and packaged using Gigapack III
 Gold packaging extracts. Plasmids containing cDNA inserts
 were excised from the recombinant lambda-zap phage using
 Ex-assist helper phage and propagated in XL04 cells."

ORIGIN

Query Match

Best Local Similarity 6.6%; Score 35.2; DB 12; Length 339;
 Matches 105; Conservative 0; Mismatches 73; Indels 6; Gaps 2;

QY 34 AGCTCCGGGGGAAATAGCGTGTCTGCTAATGCTTGTGATATCATGCTT 93
 Db 48 ACCGCGCGCGCGATTCACCGCTCTCTCCGCTCGAGATTCGTATCAT 106
 QY 94 GCTTGCTTACCGCCCATTTGATATATTT-----CGGTATATCATTTCTCGGAA 148
 Db 107 GACTCCGATCCAGCTATTGATGATATCTTCTAGCCTGAATTCATGCTGAT 166
 QY 149 TGGGATCAAGAGCAGCTCATTAACATTAAGAAATGTTGTGAAGCAAGATCA 208
 Db 167 TTCTGATGAAGAGCATGATCATGAACGTGAATTAATGATCATGATTTGATCATGA 226
 QY 209 GACC 212
 Db 227 GAAC 230

RESULT 12

BH567971
 LOCUS

DEFINITION BH567971 BOGH Brassica oleracea genomic clone BOGH05, genomic
 survey sequence.

ACCESSION BH567971

VERSION BH567971.1 GI:17819811

KEYWORDS GSS

SOURCE Brassica oleracea

ORGANISM

REFERENCE
 AUTHORS Grusak M.A., Samac, D.A., Town, C.D., Van Aken, S., Uterback, T.,
 TITLE Cho, J. and Fraser, C.M.
 JOURNAL Whole genome shotgun sequencing of Brassica oleracea
 COMMENT Unpublished (2001)

Contact: Michael A. Grusak
 USDA/ARS Children's Nutrition Research Center
 Baylor College of Medicine
 1100 Bates Street, Houston, TX 77030-2600, USA
 Tel: 713-798-7044
 Fax: 713-798-7078
 Email: mgrusak@bcm.tmc.edu

71GR sequence name: MTOA006TK

More information is available at: www.medicago.org
 Seq primer: TF
 Class: sheared ends.

Location/Qualifiers

FEATURES

source

1..595
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOGH05"
 /clone_lib="BOGH"
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match

6.6%; Score 35.2; DB 28; Length 595;

Best Local Similarity 58.7%; Pred. No. 14;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 114 TACTGATATATTCGCTGATATCATTTTCGGATGCGATCAAGACGAGCTCATTA 173
DB 37 TACAAAGTTTACGACGAGGAGTAATTTTCATATCTTATCAAGAGTAGACATTAAC 96
QY 174 CCATTAAGGAAATGTTTGTGAAGCAGATCAGACCACTTG 217
DB 97 ACAACATCAATATTTTCGAAAGAAAGATATACGAGCTTTG 140

RESULT 13
BZ069169/c
LOCUS
DEFINITION BZ069169 798 bp DNA linear GSS 10-OCT-2002
1kh07g11.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION BZ069169
VERSION BZ069169
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 798)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: rk.wilson@wustl.edu
Plate: 1kh07 row: 9 column: 11
Seq primer: -21UPOT forward
Class: shotgun
High quality sequence start: 67
High quality sequence stop: 508.
Location/Qualifiers
1. 798
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: POTW13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T0100DH3 buds, provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 6.6%; Score 35.2; DB 28; Length 798;
Best Local Similarity 60.4%; Pred. No. 15;
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 84 AATCATGCTTGTGCTTACCGCCGATCTACTGATATATTTGCTGATATCTTCT 143
DB 472 AATCATGCTTGTGCTTATTTATCAAGCCATTTTGAAGATATTCGTGATATCATATG 413
QY 144 CGGAATCGCATCAAGACGAGCTCATTAACCATTA 179
DB 412 CTGAATTTAAAAAAAATTCATTCATTA 377

RESULT 14
CG928645/c
LOCUS
DEFINITION CG928645 852 bp DNA linear GSS 12-DEC-2003
MBHFJ36TR mch2 Medicago truncatula genomic clone 55E24, genomic
survey sequence.
ACCESSION CG928645

VERSION CG928645.1 GI:39790532
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 852)
Town,C.D., Shetty,J., Koo,H. and Feldjlyum,T.F.
Sequencing of BAC ends from Medicago truncatula
Unpublished (2003)
Other GSSs: MBHFJ36TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: TGTAAACGACGGCAGT
Class: BAC ends.
Location/Qualifiers
1. 852
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/clivax="genotype A17"
/db_xref="taxon:3880"
/clone_lib="55E24"
/note="Vector: pBelOAC11, site 1: HindIII, site 2:
HindIII; Cook, D.R. and Kim, D.J, unpublished"

ORIGIN
Query Match 6.6%; Score 35.2; DB 29; Length 852;
Best Local Similarity 47.7%; Pred. No. 16;
Matches 103; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 111 TTGACTGATATATTCGCTGATATCATTTTCGGATGCGATCAAGACGAGCTCAT 170
DB 611 TTTTCTTTATATACGCTCTTAATCAACTTTTGTGTTCTTCTATAGTAATGCTGAC 552
QY 171 AAACATTAAGAAATGTTTGTGAAGGACACATCAGACCACTTGACCATCATCA 230
DB 551 GTGAGAGAAAGATGATGCTTGAGTGAACCTGTGCTGACCGCAATCAAAAACA 492
QY 231 CGAACAACGACGAGATGAACTTATCTACTGACCAATGTTTAAAGGCAATGCTAT 250
DB 491 CGAGCAAAAGTTGAAACACTGCTGATGATGACCAATGAAAGTAAAGTCTCATATCTC 432
QY 291 CTTCCATGAGGAAATGTCATGCAACATCCCTGTA 326
DB 431 AATCCCTATAGGCCAAGTTGCTCCCAATATCTGTA 396

RESULT 15
CNS00L9Z/c
LOCUS
DEFINITION CNS00L9Z 962 bp DNA linear GSS 02-JUN-1999
Drosophila melanogaster genome survey sequence TERT3 end of BAC:
BACR24H08 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL068054
VERSION AL068054.1 GI:4958184
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 962)
Genoscope.
Direct Submision
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

SOURCE

1..962
 location/Qualifiers
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR24H08"
 /clone_lib="RPCI-98"
 /note="End : TET3"

ORIGIN

Query Match 6.6%; Score 35.2; DB 29; Length 962;
 Best Local Similarity 27.7%; Pred. No. 17;
 Matches 46; Conservative 52; Mismatches 68; Indels 0; Gaps 0;

```

QY 102 TAGCGGCATGTACTGATATATTTCGCGATATCATTTTCGGAATCGGCATCAAG 161
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 943 TATTCAGCAGVTRMMWTKGKTTWTTTGTAGKTTTAMGKRAKAAAGAAAGCCAMAHVR 884

QY 162 CAGGCTCATAAACCATAAAGAAATGTTTGTGAGGCAAGCATCAACCACTTGACCC 221
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 883 MASITTCMTMMAMAMAAATGMCYTKKRWMAAACAATTGTAATAATGGKCMRM 824

QY 222 ATCCAATCAGCAACAAACAGAGATCGAATCATATCATCTAGACCA 267
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 823 AKRAAGSWDNTATWMCDCCKRATAAABMAAMWAATDGAIVCA 778
  
```

Search completed: May 25, 2004, 02:57:39
 Job time : 2504 secs